

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2000, 18:25:29 : Search time 23795.2 seconds
(without alignments)
1132.312 Million cell updates/sec

Title: US-09-227-881-3
Perfect score: 6169
Sequence: 1 atcttggtcagttacatc.....cttggtccctccatgtag 6169

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1033670 seqs, 2183789903 residues

Total number of hits satisfying chosen parameters: 2067340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba1: *
2: gb_ba2: *
3: gb_om: *
4: gb_ov: *
5: gb_pat: *
6: gb_ph: *
7: gb_pl1: *
8: gb_pl2: *
9: gb_pl3: *
10: gb_pl4: *
11: gb_pl5: *
12: gb_pl6: *
13: gb_pl7: *
14: gb_pl8: *
15: gb_pl9: *
16: gb_pl10: *
17: gb_pl11: *
18: gb_pl12: *
19: gb_pl13: *
20: gb_pl14: *
21: gb_pl15: *
22: gb_pl16: *
23: gb_pl17: *
24: gb_pl18: *
25: gb_pl19: *
26: gb_pl20: *
27: gb_pl21: *
28: gb_pl22: *
29: gb_pl23: *
30: gb_pl24: *
31: gb_pl25: *
32: gb_pl26: *
33: gb_pl27: *
34: gb_pl28: *
35: gb_pl29: *
36: gb_pl30: *
37: gb_pl31: *
38: gb_pl32: *
39: gb_pl33: *
40: gb_pl34: *
41: gb_pl35: *
42: gb_pl36: *
43: gb_pl37: *

44: em_htg7: *
45: em_htg8: *
46: em_htg9: *
47: em_htg10: *
48: em_htg11: *
49: em_htg12: *
50: em_htg13: *
51: em_htg14: *
52: em_htg15: *
53: em_htg16: *
54: em_htg17: *
55: em_htg18: *
56: em_htg19: *
57: em_htg20: *
58: em_htg21: *
59: em_htg22: *
60: em_htg23: *
61: em_hum3: *
62: em_hum4: *
63: em_hum5: *
64: em_hum6: *
65: gb_pl5: *
66: gb_pl6: *
67: gb_pl7: *
68: gb_pl8: *
69: gb_pl9: *
70: gb_pl10: *
71: gb_pl11: *
72: gb_pl12: *
73: gb_pl13: *
74: gb_pl14: *
75: gb_pl15: *
76: gb_pl16: *
77: gb_pl17: *
78: gb_pl18: *
79: gb_pl19: *
80: gb_pl20: *
81: gb_pl21: *
82: gb_pl22: *
83: gb_pl23: *
84: gb_pl24: *
85: gb_pl25: *
86: gb_pl26: *
87: gb_pl27: *
88: gb_pl28: *
89: gb_pl29: *
90: gb_pl30: *
91: gb_pl31: *
92: gb_pl32: *
93: gb_pl33: *
94: gb_pl34: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	6105.4	99.0	79376	65	HS454G6
2	6054.4	98.1	170425	77	AC024490
3	5300	85.9	5300	11	AF007562
4	2677.4	43.4	2800	66	HSXOC1
5	1190.4	19.3	1228	9	AB006686S1
6	1084.4	17.6	1086	66	HSGLC1A1
7	651.2	10.6	1934	35	D88214
8	640.4	10.4	1999	5	AR030962
9	640.4	10.4	1999	5	AR060082
10	640.4	10.4	1999	5	AR060089
11	640.4	10.4	2000	66	HS05257
12	640.4	10.4	2002	5	AB4847

13	635.6	10.3	2000	5	A84850	Sequence 2
14	626.4	10.2	2061	66	HS4F001620	AF001620 Homo sapi
15	604.4	9.8	1512	5	A84848	Sequence 3
16	604.4	9.8	1512	5	AR030963	Sequence 3
17	604.4	9.8	1512	5	AR066023	Sequence 3
18	604.4	9.8	1512	5	AR069090	Sequence 3
19	599.6	9.7	1512	5	A84851	Sequence 3
20	585.8	9.5	2800	12	MMWYOC1	AF049794 Mus muscu
21	559	9.1	1016	12	MMWTCGP1	AF041333 Mus muscu
22	556.6	9.0	1969	5	AR020502	Sequence 2
23	556.6	9.0	1969	5	AR020503	Sequence 3
24	519.6	8.4	1491	5	I36471	Sequence 3
25	519.6	8.4	1491	5	AB013592	Mus muscu
26	440.8	7.1	2004	12	AF039869	Mus muscu
27	440.8	7.1	2004	12	AF039869	Mus muscu
28	430.4	7.0	2044	12	AB019393	Rattus no
29	426.2	6.9	2068	12	AF093567	Rattus no
30	398.8	6.5	1473	3	AB027758	Bos tauru
31	217	3.5	228	11	AF007564	Homo sapi
32	189.8	3.1	161577	10	AC007688	Homo sapi
33	189.8	3.1	193123	77	AC023790	Homo sapi
34	189	3.1	199722	71	AC012404	Homo sapi
35	187.8	3.0	97037	9	AC004973	Homo sapi
36	187.8	3.0	135038	67	HDWYMXD703	L78810 Homo sapien
37	185.8	3.0	76727	65	HS821D11	Human DNA
38	185.8	3.0	152044	79	AC026395	Homo sapi
39	185.8	3.0	157057	78	AC025947	Homo sapi
40	185.8	3.0	161499	72	AC015488	Homo sapi
41	185.8	3.0	184656	86	AL161726	Homo sapi
42	185.6	3.0	200681	69	AC008755	Homo sapi
43	185.6	3.0	201372	86	AL157941	Homo sapi
44	184.8	3.0	146190	89	AP001813	Homo sapi
45	184.8	3.0	163494	89	AP002391	Homo sapi

ALIGNMENTS

RESULT 1
LOCUS HS454G6/c
DEFINITION Human DNA sequence from PAC 454G6 on chromosome 1q24. Contains triabecular meshwork inducible glucocorticoid response protein, TIGR, myocillin, ESTs and STRs.
ACCESSION 298750
VERSION 1
KEYWORDS 1q24; myocillin; TIGR.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 79376)
AUTHORS Deadman,R.
TITLE Direct Submission
JOURNAL Submitted (27-OCT-1997) Chromosome 1 Project Group
(http://www.sanger.ac.uk/HGP/Chr1/) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquires: hamquerry@sanger.ac.uk
COMMENT
On Feb 14, 1998 this sequence version replaced g1:2465060.
IMPORTANT: This sequence is not the entire insert of clone 454G6. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variations annotated may not be found in the sequence submission corresponding to the overlapping clone as we submit sequences with only a small overlap as described above.
This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre chromosome 1 mapping group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr1/

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.
The true left end of clone 454G6 is at 1 in this sequence. The true left end of clone 560B9 is at 79273.
454G6 is from the library RPC13 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong.
For further details see <http://bacpac.med.buffalo.edu/>.

FEATURES

source
1..79376
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1q24"
/clone="RP3-454G6"
/clone="11b-RPC1-3"
435..472
/note="19 copies of 2 mer 82 & conserved"
prim.transcript 1914..>3968
/note="match: multiple ESTs
match: R56676 AA043968 W63639 F12081 AA046699
match: F02925 AA131540 W00634 R36066 AA313383
match: AA163561 F02925 AA131540 W00634 R36066
match: AA131383 AA163561 N89173 AA174814 AA057059
match: AA329084 W47082 AA043955 AA414183 AA333681
match: AA046487 AA369741 H08313 AA186895 H32730
match: H08353 H08236 N42052 D61944 R27102 N32353
match: N30491 AA307150 AA1922
3703..3746
/note="22 copies of 2 mer 89 & conserved"
4051..4183
/note="Alusg repeat: matches 1..133 of consensus
incomplete repeat"
4200..4502
/note="Alusg repeat: matches 2..301 of consensus"
4659..4851
/note="Alusg repeat: matches 2..194 of consensus
incomplete repeat"
5216..5345
/note="Aluud repeat: matches 132..1 of consensus
incomplete repeat"
7759..7907
/note="MIR repeat: matches 174..1 of consensus"
7933..9328
/note="TIGER1 repeat: matches 1..1472 of consensus"
9332..9626
/note="Alusg repeat: matches 1..289 of consensus"
9639..10335
/note="TIGER1 repeat: matches 1469..2174 of consensus"
10343..10642
/note="Alusg repeat: matches 1..300 of consensus"
10643..10856
/note="TIGER1 repeat: matches 2175..2417 of consensus"
<10903..>16855
/note="endogenous retroviral sequence"
10949..11384
/note="LRR2 repeat: matches 31..449 of consensus"
15835..15870
/note="18 copies of 2 mer 83 & conserved"
16856..17286
/note="LRR2 repeat: matches 31..449 of consensus"
17287..17574
/note="Alusg repeat: matches 15..300 of consensus"
18294..18650
/note="THE1B repeat: matches 358..1 of consensus"
18877..19180
/note="Alu repeat: matches 301..2 of consensus"
19767..20013
/note="MIR2-internal repeat: matches 5002..4750 of consensus"

```
repeat_region /note="MLT1F repeat: matches 539. .471 of consensus"
20051..20118
repeat_region /note="Aluub repeat: matches 131. .1 of consensus
20130..20261
Incomplete repeat"
repeat_region /note="MLT1F repeat: matches 482. .1 of consensus"
20264..20722
repeat_region /note="MLT1F repeat: matches 482. .1 of consensus"
20858..21223
repeat_region /note="MSTD repeat: matches 394. .1 of consensus"
21216..21302
repeat_region /note="MLT2_internal repeat: matches 4520. .4433 of
consensus"
21403..21703
repeat_region /note="MLT2_internal repeat: matches 3887. .3580 of
consensus"
21978..22357
repeat_region /note="MLT2_internal repeat: matches 3218. .2839 of
consensus"
22363..22524
repeat_region /note="MLT2_internal repeat: matches 2495. .2317 of
consensus"
22531..22839
repeat_region /note="AlusX repeat: matches 302. .1 of consensus"
23007..23309
repeat_region /note="AlusP repeat: matches 3. .301 of consensus"
23286..23680
misc_feature /note="STS G07544"
complement(23652..24072)
/note="STS G07436"
24008..24290
repeat_region /note="Aluud repeat: matches 298. .6 of consensus"
25895..26364
repeat_region /note="LTR2 repeat: matches 2. .449 of consensus"
26397..26697
repeat_region /note="Alusq repeat: matches 1. .302 of consensus"
26719..27021
repeat_region /note="AlusX repeat: matches 1. .302 of consensus"
29037..29334
repeat_region /note="AlusX repeat: matches 300. .3 of consensus"
30028..30310
repeat_region /note="AlusX repeat: matches 1. .301 of consensus"
30402..30539
repeat_region /note="MLT2B repeat: matches 264. .404 of consensus"
30402..30615
/note="MLT2A repeat: matches 264. .453 of consensus"
<30801..>31136
/note="match: 5' EST AA256902 clone 682136"
30980..31222
repeat_region /note="MER4B repeat: matches 199. .431 of consensus"
31232..31528
repeat_region /note="AlusC repeat: matches 299. .1 of consensus"
31530..31654
repeat_region /note="MER4B repeat: matches 417. .540 of consensus"
31836..32135
repeat_region /note="Aluy repeat: matches 300. .1 of consensus"
32200..32301
repeat_region /note="Aluud repeat: matches 186. .287 of consensus
Incomplete repeat"
32365..32493
repeat_region /note="MIR repeat: matches 206. .67 of consensus"
33283..33399
repeat_region /note="MIR repeat: matches 77. .196 of consensus"
33408..33667
repeat_region /note="Aluy repeat: matches 1. .291 of consensus"
33956..34043
/note="MIR repeat: matches 80. .167 of consensus"
34725..34904
/note="Aluud repeat: matches 299. .127 of consensus
Incomplete repeat"
34907..35207
repeat_region /note="Aluy repeat: matches 300. .1 of consensus"
35212..35344
repeat_region /note="Aluub repeat: matches 133. .1 of consensus
```

```
Incomplete repeat"
repeat_region /note="Aluud repeat: matches 299. .1 of consensus"
36545..36842
repeat_region /note="MER3 repeat: matches 209. .13 of consensus"
38190..38379
repeat_region /note="AlusX repeat: matches 1. .302 of consensus"
38382..38682
repeat_region /note="AlusX repeat: matches 145. .2 of consensus"
38386..38968
repeat_region /note="MIR2 repeat: matches 3. .296 of consensus"
38983..39279
repeat_region /note="Aluub repeat: matches 354. .2 of consensus"
39418..39773
repeat_region /note="THE1A repeat: matches 354. .2 of consensus"
39775..40120
/note="THE1B-INTERNAL repeat: matches 1580. .1234 of
consensus"
40757..41023
repeat_region /note="Aluud repeat: matches 37. .301 of consensus
Incomplete repeat"
41307..41589
repeat_region /note="Alusq repeat: matches 21. .303 of consensus

Query Match 99.0%; Score 6105.4; DB 65; Length 79376;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 6165; Conservative 0; Mismatches 1; Indels 9; Gaps 5;

QY 1 attctgttcagttaccctcagggcctattatgaatgaatgataaccatgtgaag 60
|||||
Db 68406 ATTCTGTTCAGTTTACCTCAGGGCTATTATGAAATGATTAACCAATGTGAAG 68347

QY 61 tccataaactgtatagccctccatcgtatgtagtctcttggagaagatgataagaatca 120
|||||
Db 68346 TCCATAAAGCTGATATAGCCCTCATTCGGATGATGCTTTGGCAGATGATAAGATCA 68287

QY 121 ggaagaagaagatccacgttagcgaagtgccaggtcgtgtctctattttgtga 180
|||||
Db 68286 GGAAGAAGAGATATCCACGTTACCAAGTCCAGGCTGTCTCTTATTTTGTGA 68227

QY 181 cagattgtctctcagagaagctattcttcagagaacatccatatgataatc 240
|||||
Db 68226 CAGATTGTCTCTGACAGAGCTATTCTTCAGGAACATCAATCATATGTTAATC 68167

QY 241 catcaaaacgaagcctaagaacagaaatgagatggcacttggcccaagaaatgccag 300
|||||
Db 68166 CATCAAAACGAGACTTAAGAACAGAAATGAGATGGCAGCTGCCCAAGAAATGCCAG 68107

QY 301 gagagcaaatatgatgataaataaaccttccctctgttttaatttcagaaaaatg 360
|||||
Db 68106 GAGAGCAAAATGATGAAATAAATTAATCTTCCCTTGTTTTAAATTCAGAAAAATG 68047

QY 361 atgaagacaaaatcaatgataaggaagaacagctcagaagaagaatgttccaaattgg 420
|||||
Db 68046 ATGAGACCAAAATCAATGATATAGGAAGAACACTCGAAGAAAGATGTTCCAAATTGG 67987

QY 421 taattaaatattgtctccttgggaagaagacctcatgtagcttgaatgggaaatggaa 480
|||||
Db 67986 TAATTAAATATTGTTCCTTGGGAGAGACCTCATGTAAGCTTGATGGCAAAATGGAA 67927

QY 481 aaacgtcaaaagcatgcatcgcagatcccaagtgatattatlttaaaacacagat 540
|||||
Db 67926 AAACGTCAAAAGCATGTCATCGATCCCAAGTGATATTATTTTAAAAACCGAT 67867

QY 541 ggcatacctctggggaggaagtcaggaagtcacgtttagtaaaagagacataaacaat 600
|||||
Db 67866 GGCATACCTCTGGGAGGAGCAAGTTCAAGAGGTGATGTTAGCAAAAGCACATTAATAC 67807

QY 601 agcaaaatcaaaatccgcacaatgcaggagaaatggggacccgggaaagccttcaaac 660
|||||
Db 67806 AGCAAAATCAAAATTCGCCAAATGCAGAGAAATGGGACATGGGAAACCTTCAATAC 67747

QY 661 agtgattaggcagttgacatgttgcacaacctcccgctctatccagggaacacaaa 720
|||||
Db 67746 AGTGATTAGGCAAGTTGACATGTTGCCAACACCTCCCGCTATACAGGGAACACAAA 67687
```

Oy 721 attgactggcctaagccctggactttcaagggaataatgaaaaactgagagcaaaacaa 780
| | | | |
Db 67686 ATTGACTGGGCTAAGCCCTGAGATTTCAGAGGAAATATGAAAACATGAGACGAAACAAA 67627
Oy 781 gacatggttaaaaggcaacccagacatgtgagccctcaaaagcagtgcccccaaga 840
| | | | |
Db 67626 GACATGGTTAAAGGCAACGAGAACATGTGAGCCTTCAAGGACACAGTGGCCCTCACGA 67567
Oy 841 gggagcccggaagccatttcccttagaaggccagtttcttaaggaaacttaaggaaactc 900
| | | | |
Db 67566 GGGAGCCCTGAGGCACTTTCCTTAGAAGGCCAGTTTCTTAGGAAATCTTAGAAGAACCTC 67507
Oy 901 ttgaaagatcattgaaatttaaaccaatttaagatataaaacaatactgcatgataatcag 960
| | | | |
Db 67506 TTGAAAGATCATGAAATTTTAACCATTTTAAGTATAAACAATATGCGATGATATATCAG 67447
Oy 961 tttagacatgggtcccaattttataaagtcaggcatacaagatacgtgtccagctcc 1020
| | | | |
Db 67446 TTTAGACATGGGTCCCAATTTTATTAAGTCAGGCAATACAGGATTAACGTGCCAGCTCC 67387
Oy 1021 ggaatagtcagaataatcatatagaatactgtgtcccaacttcccaacttttcagaaatgtc 1080
| | | | |
Db 67386 GGATAGGTCAAAATCATTAGAAATCACTGTGTCCCATCTTAACCTTTTCAGAAATGATC 67327
Oy 1081 tgtcaaaagccctcacacacagagcccgatgtgtgacctacaacacatactacaacccaa 1140
| | | | |
Db 67326 TGTATACCCCTCACACACAGGCCCGATGTGTCTACCTACACACATCTTAACACCCAA 67267
Oy 1141 gtgcctcaaacattgtttaacgtgtcatctcagtaagtcaccatlaacaatgccaactccc 1200
| | | | |
Db 67266 GTGCCTCAACCATTTGTTAACGTGTCTCATCTAGTAGTCCCATTAACAAATGCGACCTCCCC 67207
Oy 1201 gtgtgagagcccaatcccgctccacagaaagttcccaactctgaccttgcatacaagatgt 1260
| | | | |
Db 67206 TGTGAGGCCATCCCGCTCCACAGGAAGTCTCCCATCTTAACCTTGTGACATCAGAGATGT 67147
Oy 1261 taacagccagaagctcgtgaaaggtcgtgtctctcaaccatactgatactgtctaac 1320
| | | | |
Db 67146 TACAGCCAGAAGCTCCGTAAGGGTGTGTCTTACACATCACTGATGATCTAAC 67087
Oy 1321 acctgagctcaactgcaacctctgctcccaaggtccaagaactctcctgtctcagctccc 1380
| | | | |
Db 67086 ACCTGAGCTCACTGCAACCTCTGCTCCAGGTTCAAGCAATTCCTGTCTCACCTCC 67027
Oy 1381 cgcgttagctggactacacagagcgcaagcccggttaattttgattgttagtaagaatgg 1440
| | | | |
Db 67026 CGCGTAGCTGGAGCTACAGGGCGCACGCCGCTAATTTTGTATTGTATGATGAGATGGG 66967
Oy 1441 gttcaacataatagcccgctgtgtcttgaactccttgaccccaagtgatcccaacccctc 1500
| | | | |
Db 66966 GTTTCACCATTTTACGCCGGCTGTGTGAACTCCTGAACTGAGTGAATCCACCACTC 66907
Oy 1501 agcctcctaaagtcgtggaatbatagacagatgaatcagcgccgagcaagggctcagtgt 1560
| | | | |
Db 66906 AGCCCTCTAAAGTGTGGGATTTACAGCATGAGTCAACGCCGCCGCAAGGATCAGTGT 66847
Oy 1561 ttaataaagaataaacttgaatgggtttactaaaccaaaggaagaaagcaaaagtgtga 1620
| | | | |
Db 66846 TTAATAAGGAATTAACCTTAATGTTTACTTAACCAACAGGGAAGAAAGCAAAAGCTGTGA 66787
Oy 1621 taatttcagggaattcttggaatggaatgtgtgcatagctgtcgtctagttcccaagac 1680
| | | | |
Db 66786 TAATTTCAGGATTTCTTGGGATGGGGAATGGTGCATGAGCTGCTGCTAGTCCAGAC 66727
Oy 1681 cactgttcctcatcaacttcttctccctcaactcctcaatttcaaggctaaagttaaccattat 1740
| | | | |
Db 66726 CACTGTGCTCATCACTTTCTTCCCTCATCTCATTTTCAGGCTAAGTTACCATTTTATTT 66667
Oy 1741 caccatgctttctgtgtgaagctcacaatcgttactgaataagaagtatacaataaactag 1800
| | | | |
Db 66666 CACCATGCTTTTGTGTGAAGCTCCACATCGTTACTGAATAAGATATACATAAAGTAG 66607

Oy 1801 ttccatttggggccatctgtgtgtgtataggggaagggcatalaccgccagagactcct 1860
| | | | |
Db 66606 TTCCATTTTGGGGCCATCTGTGTGTGTATAGGGAGAGGAGGCATATCCCCAGAGACTCCT 66547
Oy 1861 tgaagcccccggcagaaggttccctctcaagcttggggagagccctgcaaacacccggggctc 1920
| | | | |
Db 66546 TGAAGCCCCCGGCAAGGTTTCTCTCCAGTGGGGAGGCCCTCGAACACCCGGGGTCC 66487
Oy 1921 tgggtgtcctgagcaacctgtcagcccggtgcacatgtgttcttctcaactcttag 1980
| | | | |
Db 66486 TGGGTGTCTGAGCAACCTGCCAGCCCTGCCACAGTGTGTTTGTATACCTCTCTAG 66427
Oy 1981 gacctgttcttcaatttctgtgtgacgtgtcaatcaaccaggaatcattgaaact 2040
| | | | |
Db 66426 GACCTGTGCTTTCATTTCTGTGTGACTCGTTCATTCATTCAGGCAATTCATTGCAAT 66367
Oy 2041 tatgtagtaactatatactgtccagacacacaggaacaaatlgltgtgacagaagtaacagc 2100
| | | | |
Db 66366 TATTGAGTACTTATATCTGCGACAGACACGACAAATGCTGAGCAAGATCTACTGC 66307
Oy 2101 cctaacctctgtggaaggtgacaagttctcatgtgaagagctgtcagaagaataatlaatagca 2160
| | | | |
Db 66306 CCTACTCTGTGAGAGTACAGTTCATCTCATGGAAGACCTGCAGAAAGAAATTAATAGCCA 66247
Oy 2161 gccaaactaaacccagtgctgaaagaagaataaacaacacacttgaagaattgtgcgc 2220
| | | | |
Db 66246 GCNAACCTTAACCCGAGTCTGAAGAAAGAAATTAACACCATCTTGAAGATGTGCGC 66187
Oy 2221 agcatcccttaacaaagagccacctcctcctagcccccctgtcctccatcgtgtccggagg 2280
| | | | |
Db 66186 AGCATCCCTTAACAAGGCGACCTCCCTAGCCGCCCTCTCTCTCAATGATGCGGAGG 66127
Oy 2281 ccccgaagcccgagctcttcccaagcctcctccatcaatcagacagcgctcagctgtgct 2340
| | | | |
Db 66126 CCCCCAAGCCGAGTCTTCAAGCTCTCTCTCATCATGATCAGAGCGCTGCAGCTGCGCT 66067
Oy 2341 gctctgctcccgtyaactgtctcgtgtgtcatctagctgtgagactccttgcctcaggct 2400
| | | | |
Db 66066 GCCTGCTTCCCGTGAATCGTCTGTGTCATCTGCTGAGCTGAGAGCTCTTGCTCCAGCT 66007
Oy 2401 ccagaagaagaatggaaggggaataactagttcaacggaatactggaagggagcagtgctc 2460
| | | | |
Db 66006 CCAGAAAGGAATGAGAGGGAAGAACTATACGCAAGAACTGAGGGGACAGTGTTC 65947
Oy 2461 ctcaagagggaaggggcttccacagtcacaggaatctccaggaaggttggagacttgcagggag 2520
| | | | |
Db 65946 CTCAGAGGAAGGGGCTCCACAGCTCCAGAGAAATCCAGAGAGTGGGACTGCAGGGAG 65887
Oy 2521 tggggaagcgtggggctgagcggtgtctgaaagcaaggaaggtgaagaggcaaggtcgaa 2580
| | | | |
Db 65886 TGGGAGCCCTGGGCTGAGCGGTGCTGAAGGCAAGAGGTGAAGAAAGGCAAGGCTGAA 65827
Oy 2581 gctgcaccaatgttcaagtggtgttcaaggggctgggaatttccgtgtcttccgtgtgagc 2640
| | | | |
Db 65826 GCTGCCAGATGTTCAGTGTTCACGGGCTGGGAATTTTCGTTCTCTCTGTGAGCG 65767
Oy 2641 ctcttattcttctcgtctggaaggaagaatctcattcaagaaggaatgcaagttc 2700
| | | | |
Db 65766 CTTTATCTTTCTCTCTGCTGAGAGGAAGAAGCTATTTTCATGAAGAGATGCAAGTTTC 65707
Oy 2701 ataaagtcagctgttaaaattccaaggtgtgtgcatgtgttcttccctcacgaagcccttat 2760
| | | | |
Db 65706 ATAAAGTCAGTGTAAATAATCCAGGGGTGCATGGGTTTCTTCAAGAGAGCCCTTAT 65647
Oy 2761 ttaattgggaataatgaagcgaagctcatcttccctagggccgtttaatctcaaggaagaagtgaac 2820
| | | | |
Db 65646 TTAATGGGAATATAGAGGCAAGCTCATTTCTAGGCGGTAAATTCACAGGAGAAAGTATAC 65587
Oy 2821 tggagcttcttctcctcaaggttctcgtgcaactactcaagccctgtgtgtgagacttggacta 2880
| | | | |
Db 65586 TGGAGTCTTTCTTTCATCATGTCTTCTGGGCAACTACTACGCCCTGTGTGTGACTTGGCTTA 65527
Oy 2881 tgcagaagcgttcgaaaaaccttgaaatcaggaagactcgglttcttcttctgttctgtccalt 2940

Dd	65526	TGCAGACGGTTCGAAACCTTGGAAATCGAGAGACTCGGTTTCTTTCTTGTTCTCCATT	65467
Qy	2941	ggttcgcgtgcgacgcgtgagcaagtgctctcccttcccttggccatagctctctcgt	3000
Dd	65466	GGTTGCGTGTGGACCGTGGCGCAAGTGTCTCTCTCCCTGGCCATAGTCTTCTGCT	65407
Qy	3001	ataaagacccttgcaagctctcgtgtctctgtgaacacctccctcgtatctctcgtgaggg	3060
Dd	65406	ATTAAGACCCTTGCAGCTCTCTGTTCTGTGAAACCTTCCCTGTAATTCCTGTGAAGGG	65347
Qy	3061	ggaatttgagagggaagaaaggcaaaagctcgmgacgcttgagccaaagggaagtgtgaagg	3120
Dd	65346	GGATGTTGAGAGGGGAAGAGGACAGAGCTGGAGCACTGAGCCACAGGGGAAGTGGAGGG	65287
Qy	3121	ggaacgaaggaagcagagcagaagcttggtgtctccacaagctccacgatacagtcagacbc	3180
Dd	65286	GCACAGGAAGGACGAGCAGAACTGGGTGCTCCATCAGTCTACGTATCAGTCACTGAGACTC	65227
Qy	3181	caggaaccgaagaccaabgcttcagaaagctcctaagaaaccacaagcacattccct	3240
Dd	65226	CAGGACCGGAGCCCAAAATGCTTACAGGAAGCTCAATGAACCAACAGCCACATTTTCTCT	65167
Qy	3241	tccccaagcatatgacaatggcatttgcacataacaaaagaatgcagaactaaactgct	3300
Dd	65166	TCCCTTAGCGATTGACAAATGGCAATTTGGCAATTAACAAAAGAAATCAGAGCAATCTGCT	65107
Qy	3301	ggtagctttgccttgccatccaacactggccagagcaagctggaaaatgycagaagctg	3360
Dd	65106	GCTTACTTTTGGCTTGCTGCAATTCAAAACCTGGCCAGACAGCATGTGAAATGCCAGAGATTG	65047
Qy	3361	tcaaaccttccacccttgaccagaaccccacgcagctcagcaatgactcgtgcagacag	3420
Dd	65046	TTAACCTTTACCCCTGACCCAGCACCCCAACGACGCTCAGCACTGACTGTGACACACGG	64987
Qy	3421	agtgaccgtcagcgcaggggaggaagaagaagaagaggaatgatatgacaaagaag	3480
Dd	64986	AGTGACTGTGCACCGACGGGAGAGAGAAAGAGAGGGAATGCTATGACCAAGAAAG	64927
Qy	3481	acaagattcaataaaggcaggtgggaattacaacagagggttatagtcacgctgacccctg	3540
Dd	64926	ACAGATTCCTTCAAGGGCGGTGGGAATTCACACAGGGATTAATGATCCACGAGTCTGG	64867
Qy	3541	gttcataggagcagggtctatctctggtggggaaaaaatacagctccaagggaaatcgsgaa	3600
Dd	64866	GTTCTTAGAGGCGAGGGCTTAATTTGGGGGAAAAAATAGTTCAAGGAATCCGGAGA	64807
Qy	3601	ccgtgattctaaactataatttcccttacaagctgagtaattctgacaagctcacag	3660
Dd	64806	CCTGATTTCTAATACTAATTTTTCCTTTACAGCAAGTAAATTTGACAGCAAGTACAAAG	64747
Qy	3661	gtaagtacacgagagcgtgaagattactagttctctctctatctgaagacttttctcgt	3720
Dd	64746	GTAGTAACCTGAGCGCTGTAGATTACTTAATTTCTCTTAATGGAACCTTTTTCCTGT	64687
Qy	3721	ggagcttagcagcacaagggcaatcccgcttctctttaaacygaagaacatctcctaaag	3780
Dd	64686	GGAGTTAGCAGCACAGAAGCAATCCCGTTCTTTTAACAGGAAGAAACATTCTTAAGAG	64627
Qy	3781	taaaagccaacagatccaagccttaagttcttgctgactaataatgatatggtttttgaaaaat	3840
Dd	64626	TAAAGCCAAACAGATTCAAGCCTAGAGTCTTGCTGACTAATATGATTGGTTTGTGAAAAAT	64567
Qy	3841	catctcagcgaatgcttactacatctgattccaagaataagagctgatacccttggcaagctg	3900
Dd	64566	CATTTTCAGGAATGTTACATATGTGATTCGAAAATGAGACATGATCCCTTGTGACGCG	64507
Qy	3901	taaaacaaacacccagcttgaataatgctccaagctcaaggtctaaactcagaacaaatcaaa-	3959
Dd	64506	TAAACAAACCACTTTGTAAATGTCTCAAGTTCAAGCTTAACCTGCAGAACCAATCAAAAT	64447
Qy	3960	aagaaatagaactctttagagcaaaactggttctcccaactcgtgaggtgagctgcgcagg	4019

D6	64446	AAAGATACAACTTTAGAGCAAACTGGTGTTCCTCCAC - TCTGGAGGTGGAGTCTGCCAGGG	64388
OY	4020	caatttggaaabatltaacttccaaagatagacagctgttgttgaatlaacaacaataag	4079
D6	64387	CAGTTTGGAAATATTATTACTTACCAAGATATTGACACTGTGTGGTATTAAACATATAAG	64328
OY	4080	ttgtcccaaaagccaatcatatattcaagtggtctaaagttactcttgcgaagtttggcata	4139
OY	4140	tttaattgcctatcgccattgccttcttcttctcctctgggtcttaatgtaagaaga	4199
D6	64327	TTGCTCAAAAGGCATCATATTATTTCAAGGCGCTTAAAGTTACTTCTGACAGTTTGGTATA	64268
OY	4200	gggaattatlaaactcaagtlccagaagcctgtgaattgaaatgagaaaaaatalcatc	4259
D6	64207	GGGATTATTAACTTACCTACAGTCCAGAAAGCGCTGTGAATTTGAATGAGAAAAATTAACATTT	64148
OY	4260	ttgtttttaaacaacttccaactaaattaaacatttatccatttgcgaatagagccataa	4319
D6	64147	TTGTATTTCACACCTTCCTCACTAAATTTTAAACATTTTATTCATTGCGAATAGACCATAA	64088
OY	4320	actcaagttgttaaaacagtaaccgttgatcttgcattaccaaatagaatcacagacat	4379
D6	64087	ACTCAAAATGGTAAATACAGTACTCTGTGATTTTGTCAATTACCAATAGAAATACAGACAT	64028
OY	4380	tttaatacataatcaagtttgttcagatacgtttgaatgaaatattaatactcaaaact	4439
D6	64027	TTTATACATATATTACAGTGTGTGCAGATAGCTGTGAATGAAATATTATATCTCAAACT	63968
OY	4440	actttgaaattagacccttcgcgtgaatctgtttttaaacaataataaacaatgtttaa	4499
D6	63967	ACTTTGAATTAAGACCTCTCTCGACTGCTGTTTAAACATATTAAATAAACAATGTTTAA	63908
OY	4500	aatttggatatttggataatacatattcaatacaatttgttctcttggtaacatattc	4559
D6	63907	AATTTTGAATTTTGGATATATATATATATATATATATATATATTTCTTTGGTAACTATATATT	63848
OY	4560	tataataattgaaacacatcttcctcagaagaagttccccaagatttcacaaatgaagttcttg	4619
D6	63847	TATATATTGAAANAATCTTTCTGAGAAGATTTCCCAAGATTTCACCAATGAGGTTCTTG	63788
OY	4620	gcaatgcacacacacagagtaagaacctgaatttagaggtcaacaattgacaattgagctgaag	4679
D6	63787	GCATCACAACACACAGATAGTAAGACTGATTAGAGGCTTAACATTGACATTTGTCCTGAC	63728
OY	4680	atgcagaagctgaaatttagaaaagttctcccaagaatacaacagttgttttaaagctaaaggtc	4739
D6	63727	ATGCAGAAGCTGAATATTAAAGATTCTCCCAAGATATACACATTTTAAAGCTAAGGGGT	63668
OY	4740	gaaggggggaaatctgcgcctctctatagaagaagcctccctcgaagcctgtataggttgctgt	4799
D6	63667	GAGGGGGGAAATCTGCCCTTCTATAGGAATGCTCTCCCTTGAGACTCTGTAAGGTTGCTGT	63608
OY	4800	ccttgttgtctgcgtcgtgtgttatttctctctgtccctcgtacagttctbaaaggaactgtt	4859
D6	63607	CCTGTGTCTGGCGTGCCTGTTATTATTCTCTGTACCCGTGACATGCTTAAAGACTTGT	63548
OY	4860	tggatctccagttctctagcaatagtcgcgcggcaacagtcgaagttctcaatgagtttgcaga	4919
D6	63547	TGGATCTTCAGTCTCTACCAATAGGCCGCGACAGTGCAGGTTTTCATATGAGTTTGAGA	63488
OY	4920	gtgaaatgaaatataaaactagaabaatactcttgttgaatccagcacacacagtagtctctg	4979
D6	63487	GTAATGGAAATATTAACCTAGAAATATATCTTGTGTAATTCACACACACAGTAGTCTTG	63428
OY	4980	gttgaatgctgttgaacgt	5039
D6	63427	GTGTAAAGTGTGTATC - GT	63370
OY	5040	ataaggaactatatttgggtatgtgggtgcataaattgggaagttctctttaaagaagaact	5099
D6	63369	ATAGCACTATATTATGGGTATGGGTGCATTAATTTGGGATCTTTTAAAGAAACT	63310

[illegible][illegible]

```
* be preserved.
* 1 1300: contig of 1300 bp in length
* 1301 1400: gap of 100 bp
* 1401 2412: contig of 1012 bp in length
* 2413 2512: gap of 100 bp
* 2513 4147: contig of 1635 bp in length
* 4148 4247: gap of 100 bp
* 4248 5455: contig of 1208 bp in length
* 5456 5555: gap of 100 bp
* 5556 6997: contig of 1442 bp in length
* 6998 7097: gap of 100 bp
* 7098 8534: contig of 1437 bp in length
* 8535 8634: gap of 100 bp
* 8635 10164: contig of 1530 bp in length
* 10165 10264: gap of 100 bp
* 10265 10487: contig of 223 bp in length
* 10488 10587: gap of 100 bp
* 10588 12420: contig of 1833 bp in length
* 12421 12520: gap of 100 bp
* 12521 14843: contig of 2323 bp in length
* 14844 14943: gap of 100 bp
* 14944 17265: contig of 2322 bp in length
* 17266 17365: gap of 100 bp
* 17366 20071: contig of 2706 bp in length
* 20072 20171: gap of 100 bp
* 20172 23531: contig of 3360 bp in length
* 23532 23631: gap of 100 bp
* 23632 26137: contig of 2506 bp in length
* 26138 26237: gap of 100 bp
* 26238 29858: contig of 3621 bp in length
* 29859 36225: gap of 100 bp
* 36226 36325: contig of 6267 bp in length
* 36326 44015: gap of 100 bp
* 44016 44115: contig of 7690 bp in length
* 44116 49493: contig of 5378 bp in length
* 49494 49593: gap of 100 bp
* 49594 56796: contig of 7203 bp in length
* 56797 56896: gap of 100 bp
* 56897 62860: contig of 5964 bp in length
* 62861 62960: gap of 100 bp
* 62961 72552: contig of 9592 bp in length
* 72553 72652: gap of 100 bp
* 72653 83310: contig of 10658 bp in length
* 83311 83410: gap of 100 bp
* 83411 92992: contig of 9582 bp in length
* 92993 93092: gap of 100 bp
* 93093 103886: contig of 10794 bp in length
* 103887 103986: gap of 100 bp
* 103987 119418: contig of 15432 bp in length
* 119419 119518: gap of 100 bp
* 119519 136695: contig of 17177 bp in length
* 136696 136795: gap of 100 bp
* 136796 153977: contig of 17182 bp in length
* 153978 154077: gap of 100 bp
* 154078 170425: contig of 16348 bp in length.

FEATURES
      source
      1..170425
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /chromosome="1"
      /map="1"
      /clone="RP11-138F3"
      /clone_lib="RPCT-11 Human Male BAC"
      1..1300
      /note="assembly_fragment"
      1401..2412
      /note="assembly_fragment"
      2513..4147
      /note="assembly_fragment"
      4248..5455
      /note="assembly_fragment"
      5556..6997
      /note="assembly_fragment"
      7098..8534
      /note="assembly_fragment"
      8635..10164
      /note="assembly_fragment"
      10265..10487
      /note="assembly_fragment"
      10588..12420
      /note="assembly_fragment"
      12521..14843
      /note="assembly_fragment"
      14944..17265
      /note="assembly_fragment"
      17366..20071
      /note="assembly_fragment"
      20172..23531
      /note="assembly_fragment"
      23632..26137
      /note="assembly_fragment"
      26238..29858
      /note="assembly_fragment"
      29959..36225
      /note="assembly_fragment"
      36326..44015
      /note="assembly_fragment"
      44116..49493
      /note="assembly_fragment"
      49594..56796
      /note="assembly_fragment"
      56897..62860
      /note="assembly_fragment"
      62961..72552
      /note="assembly_fragment"
      72653..83310
      /note="assembly_fragment"
      83411..92992
      /note="assembly_fragment"
      93093..103886
      /note="assembly_fragment"
      103987..119418
      /note="assembly_fragment"
      119519..136695
      /note="assembly_fragment"
      136796..153977
      /note="assembly_fragment"
      154078..170425
      /note="assembly_fragment"

BASE COUNT  48243 a 34101 c 34753 g 50621 t 2707 others
ORIGIN
Query Match      98.1%  Score 6054.4;  DB 77;  Length 170425;
Best Local Similarity 99.6%  Pred. No. 0;
Matches 6155;  Conservative 0;  Mismatches 11;  Indels 14;  Gaps 8;

QY 1 accttgctcagttta--ccctcaggcctatctgaatgaaatgagataacccaatgtgaa 58
DB 63685 ACTTTGTTCACTTATCTCTACTACGAGGCTATATGAAGAATGATACCAATGTGAA 63744
QY 59 agtctataaactgtatgctcctcattcg-gatgtatgtctctggcagg--atgataaag 115
DB 63745 ACTCTATATACTGTATAGCCCTCCATCGTATGTATGCTTTGGCAGGTATGATAAG 63804
QY 116 aatcaggaagagagatctccacgctttagccaagtgctcagggtgtctgctctatttt 175
DB 63805 AATCAGAGAGAGAGATCCACGTTAGCCAGATGCCAGCTGTGTCTGCTCTTATTTT 63864
QY 176 agtcagagatgtctcctgacagaagcctatcttcaggaaacacacatccaatatgct 235
|||||
```


Db	63865	ACGACACAGATGTTGCTCCTCGACAGAAAGCATTTCTTCAGAGAAACATCACATCCAAATATGT	63924
Oy	236	aaatccatcaaaacagagcctaaagaaacagaaatgagatgaggactgtcccaaggaaaat	295
Db	63925	AAATCATCAACAAACAGAGAGCTAAGAAACAGAAATGAGATGGCAGCTTGCCCAAGAAAAAT	63984
Oy	236	gccagagagagcaaatgaatgaataaaataaacctttcccttgcttttaattcaaggaaa	355
Db	63985	GCCAGAGAGCGCAAAATAAATGATATAAAATTAACCTTTCCCTTGTTTAAATTCAGGAAA	64044
Oy	356	aaatcgcagagacccaaatacaatgaataagaaaacagctcagaaaagaatgcttccca	415
Db	64045	AAATATATGAGGCCAAATATCAATGAAATAAAGAAAACGCTCGAAAAAAGATGTTTCCA	64104
Oy	416	atggttaattaaatgatttgctcctctggagaaagacctccatgctgaagctgaatgggaaaat	475
Db	64105	ATTGGTAATTAAGTATTGTGTTCTTGGAAGAGACCTCATGTGAGCTTGATGGGAAAAAT	64164
Oy	476	gggaaaaaacgtcaaaaagcattgctcgtacagatcccaaaagtgaattatatttataaac	535
Db	64165	GGGAAAAACGTCMAAAGCATGTATCGATCAGATCCCAAAAGTGATTAATATTTAAAAAC	64224
Oy	536	cagatggagacatcctctggggaagagcaagctcagaaaggtcatgctagcaaaagacataca	595
Db	64225	CAGATGGCATCTCTTGGGGAGGCAGAAATTCAAGAAAGTCATGTTTACCAAGACATTAACA	64284
Oy	596	ataaacagcaaaaacaaaaatcccgcaaatgcaagagagaaatggggagactggaaagccttc	655
Db	64285	ATAACAGCAAAATCAAAATTCGCCAAATCGACAGAGAAATATGGGACCTGGAAAGCTTTC	64344
Oy	656	ataacagtgatctaggcaggttgacatgctcgaacaacatcccgctctatacaggagaa	715
Db	64345	ATMAACGATTAAGGACAGTGTGACCAATGTTGCGACAAACCTCCCGCTTAACCAAGGAAACA	64404
Oy	716	caaaaattgaactgggctaaagccctgaagccttcaagggaaatacgaaaaacttgaagagcaaaa	775
Db	64405	CAAAAATTGACTGGGCTTAAGCCTGGACHTTTCAAGGGAATATGAAAACATGAGACAAAA	64464
Oy	776	caaaaagacatggtttlaaaaggcaacacagaacaatttgtgaagccttcaaaagcagagtgccct	835
Db	64465	CAAAAACATGTTTAAAGGCCAACCAAGCAATTTGTGAGGCTTCAAAAGCAGAGTGCCCT	64524
Oy	836	cagcagaggaaccttgaggcaattgaccttaagaaagccagtttcttaagaaatcttaaga	895
Db	64525	CAGCGGGGACCTCGAGGCAATTTGCCCTTAAAGAAAGCCAGTTTCTTAAGGAATCTTAAGA	64584
Oy	896	aaactctgaaaatcaatgaatttaaaccttttaaggttaaaaaaaaatgtgatagcata	955
Db	64585	AACTCTTGAAAGATATGAAATTAATTAACCTTTTAAGTATAAAAACAAAATATGGAGTGCATA	64644
Oy	956	atcagctctagacatggtgtcccaatttataaagtcagagcatacaaggaataacgtgtccca	1015
Db	64645	ATCAATTTAAGAAATGGGTCCCAATTTTAATAAAGTCAGAGCATCAAGAGTAACGTGTCCA	64704
Oy	1016	gtcccggaatagtcagaatacatatgaataatcactgltgtcccaatccaaacttttcagaa	1075
Db	64705	GCTCCGGATAGGATCAGAAATCAATCTTAAGAAATCACTGTGTGCCCATCTTAACCTTTTCAGAA	64764
Oy	1076	tgaattctcatagccctcaacaacagggcccgatgtgtctgacctatacaacacatctacaa	1135
Db	64765	TGATTTGTCTATAGCCCTCAACACAGGCCCGGATGTGTGTGACCTCAACACATCTTACAA	64824
Oy	1136	cccaagtgacctaacacattggttaaggtgtcatctgaatgagtgcccatatacaatgccaac	1195
Db	64825	CCCAAGTGCCCTCAACCATTTGTTAAACGTGTCAATCTAATAGTGGTCCCATTTAACAATGCCACC	64884
Oy	1196	tccctctgcagcccatcccgctcccaacagaaagtctcccaactcagaactcttgatcac	1255
Db	64885	TCCCTGTGCAAGCCCATCCCGCTCCACAGGAAGTGTCCCCCACTGTAAAGATTGTGCATCAC	64944
Oy	1256	gacgtctacagccagaagctcgttgaagggttgaaggtctgtgtctctaaacctacgctatgc	1315
Db	64945	GATGTTTACAGCCAGAAAGCTCCCTGTAGGGGTGAAGGCTGTGTATTACACTTACTTATAGC	65004

QY	1316	ttcacactgagatcaactgcaacccctgcctcccaaggttcaagcaattctctgctctcg	1375
Db	65005	ttctaacacctgacctactgcacacccctgcctcccaaggttcaagcaattctctgctctcg	65064
QY	1376	cctcccgctgactgagactacagacgcacccagctaatcttctgattgttagtag	1435
Db	65065	cctcccgctgactgagactacagacgcacccagctaatcttctgattgttagtagag	65124
QY	1436	atggaggtttcaccaatatagcccgctggttcttgaactccctgaacctgaatccca	1495
Db	65125	atggaggtttcaccaatatagcccgctggttcttgaactccctgaacctgaatccca	65184
QY	1496	acctcaagcctcttaagaatgctgagatcttaagacatgagatcacgcgcgcgaaggtc	1555
Db	65185	acctcaagcctcttaagaatgctgagatcttaagacatgagatcacgcgcgcgaaggtc	65244
QY	1556	agtgtttaaataagaaataactctgaaatggttttaacaaaccaagaggaacagaacaaagc	1615
Db	65245	agtgtttaaataagaaataactctgaaatggttttaacaaaccaagaggaacagaacaaagc	65304
QY	1616	tgtgataatttaaggaattctctggagatggggaatggtgtgcatagagctgctcctga	1675
Db	65305	tgtgataatttaaggaattctctggagatggggaatggtgtgcatagagctgctcctga	65364
QY	1676	cagaccacatggtccctcaatacctctctccctcaatacctctcaagctcaagttacacat	1735
Db	65365	cagaccacatggtccctcaatacctctctccctcaatacctctcaagctcaagttacacat	65424
QY	1736	ttatcaccaatgctcttltgtgtgaagcctcccaataatgcttctgaataaagatataata	1795
Db	65425	ttatttccacctatcttttgtgtgaagcctcccaataatgcttctgaataaagatataata	65484
QY	1796	actagttccactttggggccatcgtgtgtgttataaggagagaggaataccccaagaa	1855
Db	65485	actagttccactttggggccatcgtgtgtgttataaggagagaggaataccccaagaa	65544
QY	1856	ctccttgaagcccccggcagagggttctctctccagctgggggaagccctgcaaacccgg	1915
Db	65545	ctccttgaagcccccggcagagggttctctctccagctgggggaagccctgcaaacccgg	65604
QY	1916	ggtctctgagtgctcctgaagaacctctcaaacccgctgcaactgttttctgttatacctc	1975
Db	65605	ggtctctgagtgctcctgaagaacctctcaaacccgctgcaactgttttctgttatacctc	65664
QY	1976	ctagggaacctgtgtcttctatcttctgtgtgaactcgttcatcatcacaaggaatcaatga	2035
Db	65665	ctagggaacctgtgtcttctatcttctgtgtgaactcgttcatcatcacaaggaatcaatga	65724
QY	2036	caatttatgtgacttatatacttgccagacaccagagacacaaaatggtgcaaaagagtc	2095
Db	65725	caatttatgtgacttatatacttgccagacaccagagacacaaaatggtgcaaaagagtc	65784
QY	2096	actgcccatacctctgtgaggtgtgacagtcttctcatgtgaagagctgcagagaagaattaac	2155
Db	65785	actgcccatacctctgtgaggtgtgacagtcttctcatgtgaagagctgcagagaagaattaac	65844
QY	2156	agccagccaactttaaaccacagatgtctgaagaagaagaataaacaacatcttgaagaatctg	2215
Db	65845	agccagccaactttaaaccacagatgtctgaagaagaagaataaacaacatcttgaagaatctg	65904
QY	2216	tggcgaagatacctctaaagaagcacaactccctcaggagccccctgcctgcctcaatgtgcc	2275
Db	65905	tggcgaagatacctctaaagaagcacaactccctcaggagccccctgcctgcctcaatgtgcc	65964
QY	2276	gagagcccccacaagcccgagcttctccaagcctcctccatcatagtcacaagcgtcgaact	2335
Db	65965	gagagcccccacaagcccgagcttctccaagcctcctccatcatagtcacaagcgtcgaact	66024
QY	2336	ggcctgctcgtcttcccgatgaatgctgtcctgtgtgcaatctgagactggaagactccttgctcc	2395
Db	66025	ggcctgctcgtcttcccgatgaatgctgtcctgtgtgcaatctgagactggaagactccttgctcc	66084

QY 2396 aggtccagaaagaaatgagagagaaactagctcaacgagaaatctggagggagcaatc 2455
|||||
Db 66085 AGGCTCCAGAAAGAAATGAGAGGGAAACTAGTCTAACGAGAAATGTGAGGGGACAGT 66144
QY 2456 gtctcccaagagaaaggggacctccacgctccaggaagaaatccaggaagctggagcaatc 2515
|||||
Db 66145 GTTCTCTCAGAGGAAAGGGGCGCTCCACGTCAGAGAAATTCAGAGAGGTGGGACATGCA 66204
QY 2516 gggagatggggagagcgtggggtctgagcgagtgctgaagagcgagaaagtgaagagggcaag 2575
66205 GGGAGTGGGGACCTGGGGCTGAGCGGGTCTGAAAGCGAGAAAGGTGAAAGGGCAAGG 66264
QY 2576 ctgaagcctggccagaaatgtacagatgtgttcacaggggctggagagtcttcgctggctcgt 2635
66265 CTAAAGCTGCCAGATGTTAAGTGTTCACGGGGCTGGGAGTTCCTGCTTCTCTG 66324
QY 2636 tgaagccttttaactctctctcgtcgttgaagagaaagaaatcattcaatgaagagatgca 2695
66325 TGAGCCCTTTATCTTTCTCTGCTTGAGAGAGAAAGTATTTTCATGAGAGATGCA 66384
QY 2696 gtctcataaagtcagcgtcttaaaaatcccaaggtgtgtcagatgtcttcctccaagaaagcc 2755
66385 GTTTCATAAAGTACGCTTAAATTCACGGGTGTGATGGTTCCTTACAGAGGCC 66444
QY 2756 ttcaatttaatggagaaataagaaagcagcctcaattccctagccgttaattcaacgaaagaa 2815
66445 TTATATTAAATGGGAATTAAGAAAGCAGCTCATTTCTTAGCCCTTAATTCACGGAAGAA 66504
QY 2816 gtgactgagatctctctctcaatgctctctcgttgcagaaactcagccctgtgtgagcttg 2875
66505 GTGACTGAGATCTTTCTTCTTCTCTGCTTGGGCACTACTACACCCTGTGTGACTTG 66564
QY 2876 gcttatgcaagaaagctgcaaaactctggaaatcaggaagaaatcgtcttccttcgtgtctg 2935
66565 GCTTATGCAAGAGCGTGAAGAACTTGAAATCAGAGAACTCGGTTTCTTCTGCTG 66624
QY 2936 ccatgtgtgctgctgagcagctgggcaagtgtctcctcctccctgggcaatgctctc 2995
66625 CCAATTTTGGCTGTGGGACCGTGGCAAGTGTCTCTCTTCCCTGGGCCATAGTCTTCT 66684
QY 2996 ctgctataaagaaacctgtcagcctcgtgtgtctgtgtgaacaatccctgtgactctcgtg 3055
66685 CTGCTATAAAGACCCCTGACGCTCTCGTGTCTGTGAACACTTCCTGTAATCTCTGTG 66744
QY 3056 aaggggagagcttgaagagggagaaagcagagcgtggagcagctgaagcccaagggagagtg 3115
66745 AGGGGGGATTTGAGAGGGAGAGGAGGACAGCTGAGCAAGCTGAGCCACAGGGGAGGTG 66804
QY 3116 gaggggagagagagagcagagcagaagctgggtgtgtcattcaatgactctcaatcaatgca 3175
66805 GAGGGGACAGAGAGGACAGGAGAGCTGGGTGCTCCATCAGTCTCTACTGATAGCTCA 66864
QY 3176 gactccagagacagagagcccaatgtcttcaggaagagctcaatgaaccccaacagccacat 3235
66865 GACTCCAGAGACGAGACCAATGTTCAAGAAAGCTCAATGAACCAACAGCCACATCT 66924
QY 3236 ttcctcccaagagatgaacaatgtgcaattgtgcaataacaaagaaatcagagactaa 3295
66925 TTCTCTTCCCTAAGCATGAGAAATGTGCAATTTGCCAATTAACCAAAAGATGAGAGACTAA 66984
QY 3296 ctgtgtgttagcttctgctcgtgcatctcaaaaactgggcagagcagaagctggaaatgycaga 3355
66985 CTGCTGTAGCTTTTGCTCTGGCATTTCAAAAACCTGGCCAGAGCAAGTGGAAAAATGCCAGA 67044
Db 67045 GATGTGTAACCTTTTCAACCTGACCAACACCCACAGCAGCTCACAGATGACTGTGACAG 67104
QY 3356 gattgttaaaacttttcaacccctgacagcaaccccaagcagctcaagcagtgactgtgtgacag 3415
67105 CAGGAGATGACCTGACCGCAGGGAGAGAAAGAAAGAGAGGATGATGACCAA 67164
QY 3476 gaaagacagatctcaatgaagggcagtggaattgacccacaggaattatagtcacagcgat 3535

Db 67165 GAAAGACAGATTCATTCAGAGGCGAGTGGGAATTGACACAGGGATTAATGATCCACGTGAT 67224
QY 3536 cctgggttctaggaagcagggcctataatgttgggggaaaaaaatcagttcaagggagatcg 3595
67225 CCTGGGTTCTAGAGAGCAGGCGTATTTGTGGGGGAAAAAATCACTTCAAGGGAAGTCG 67284
QY 3596 ggaagacctgaattcctaatactataatcttccttcaaaagctgagtaattctgagcaagtc 3655
67285 GGAGACCTGATTTCTATATATATATTTTCTTTACAGCTGAGTAATTCAGCAAGTC 67344
QY 3656 acaaggtagtaactgagcgtgtaagaatcaactagttctcctcaattaggaaccttttc 3715
67345 ACAAGTAACTAGAGCGGTGAGATTAAGTACTGTTCTTCTTATAGAACTCTTTTC 67404
QY 3716 tctgtgagtttagcagcaacaaagggcaatcccgcttctccttaacaggaagaaacattcct 3775
67405 TCTGTGAGTTTACACACAGAGGCAATCCGTTTCTTTTAAACGAGAAACATTTCT 67464
QY 3776 aagaagtaaaagcaaacagatctcaagcctaggtctgtcgaactaagatgtgttttga 3835
67465 AAGAGTAAGCCAAACAGATTCAAGCTTAGGCTGTGCTGACTATATGATTTGGTTTTGA 67524
QY 3836 aaaaatcttcagcgaatgttactatctgaatlcagaaaaatgaaactagtaacccttgtgc 3895
67525 AAATCATTTACAGCATGTTTACTATCTGATTCAGAAATGAGACTAGTACCTTTGGTC 67584
QY 3896 agctgtaaacaaacaccagctgtaaatgtctcaagtctcaagctcaacgcaagcaaat 3955
67585 AGCTGTAAACAAACACCATTGTAATGTCTCAAGTTCAAGGCTTAACTGCAACCAAT 67644
QY 3956 caaa-aagaaatagaatctttagagcaaacgtgttctccacacctcggaggtgagctgc 4014
67645 CAATATAAGATTAATCTTTAGCAAACTGTCTCTCAC-TCTGGAAGTAAAGTCTGC 67703
QY 4015 caaggcagttctggaatatctactcaacaaglaatgaacgtgtgtgtgatatcaaca 4074
67704 CAGGGCAGTTGGAATATTTACTTCAAGATGATGCACTGTGTTGATTAACACA 67763
QY 4075 taaagtgtccaaaggaatcatatctcaagtgtgcttaagttaactctcgaagtttg 4134
67764 TAAAGTGTGCAAAAGGCAACATATTTCAAGTGGCTTAAAGTTACTTTCGACAGTTTG 67823
QY 4135 gtaatttatgtgctatgtgcattgtcttcttctccttgggttcaatgta 4194
67824 GTATATTATTTGGCTATTTGCCATTGCTTTTGTGTTTTTCTTCTTGGTTATTAATGTA 67883
QY 4195 aagcaggaatlaatlaacclacagctccagaagcctgtgaattgtgaattgagaaaaatla 4254
67884 AAGCAGGATTAATTAACCTAGAGTCCAGAAAGCTGTGAATTTGAATGAGAAAAATTA 67943
QY 4255 cactttgtcttcaacaccltcaactaaatlaacaatcttaatlccaatgagaaatgagc 4314
67944 CATTGTTGTTTAAACCCCTTCACTTAATTAATTAATTTTATTCATTCGAAATGAGC 68003
QY 4315 cataaactcaaggtgtaataacagtaaccgtgtatctgtgcattacacaaatagaatcaca 4374
68004 CATTAACCTCAAGTGTAAATACAGTACCTGTGATTTTGTCAATTAACAAATGAAATCACA 68063
QY 4375 gacatttatactatlaacagttgttcagatacgtltgtlaagtgaaatlaattatactca 4434
68064 GACATTTATATATATTAACAGTTGTGACAGATACGTGTGAAGTGAATAATTTATACTCA 68123
QY 4435 aaactacttgaataatagaccctccgtgtgaactctgttcttaacacatacctaaataacatg 4494
68124 AAATCTATTGAAATTAAGACTCTCTGTGATCTTGTGTTTAAATTAATTAATTAACATG 68183
QY 4495 tttaaaaatttgatatttgataatacctaatctcatcaatctgttcccttgaatccta 4554
68184 TTTTAAATTTTGATATTTTATATATATATTTATATATCTATTTGTTTCTTTGTAATCTA 68243
QY 4555 taatttataatcttgaaataatccttcctgaaagagctccacagatctcaacaaatgaggt 4614

[illegible]

OY	5695	agcttggaacacctgtgaggggaggagcgaggccgcctcgtgaaaccacaacccaagaagtctggaga	5754
Db	69382	AGCTTGGCAACCCCTTGAGGCGGGAGCGGGACCKAGCTGTGAATCCAAACCAGAGAATTGGAGA	69441
OY	5755	ctgcctacagcaaacctccctccgagacaagtcagttctctgagaaagagaagacgactaa	5814
Db	69442	CTGCCTTACAGCAACTCCTCCGAGACAGTCAGTTCTCTGAGAAGAGAGAAGAACGACATTA	69501
OY	5815	ggcaagaataatgaaattcttggcccaggaaggtcttgaaaagcagcacagccaaggaagtaagaagc	5874
Db	69502	GCCAAGAAAATAAGATATCTGCCACAGAGCTTGGAAAGCAGCAGCCAGAGAGGTATGCAAGGC	69561
OY	5875	tgaagaaggggccaaagtgtccccagaccgagacactgtcccgggctctgtgcacaaagctcca	5934
Db	69562	TGAGAAAGGGGCCAGTGTCTCCACAGACCAGACACTGCTCGGGCTGTGTCCACACAGGCTCA	69621
OY	5935	gagaagtgtaaagaatgcagaagtcgggggagactctgtgatcaagagtgataatgctcgtagt	5994
Db	69622	GAGAAGGTAAAGATGCAGAGTAGTGGGGGACCTGTGATTCAGCAGGTGATATGGCTCGTAGT	69681
OY	5995	gaacctgtcaagggcgctccaaggctc-----cctgcgcccttctctaagagatgtcaagct	6050
Db	69682	GACCTGCTACAGGGCCCTCCAGACCTCCCTGCTGCTGCTTCTCTCAGAGACTGCACACT	69741
OY	6051	agcacaagaacagatatcatgaagaaagacaa-cgatcaccttcaagatatactaagtaat	6109
Db	69742	AGCACAAACAGATGAATTAAGAAAGACACAGCATCCTTCAAGTATTACTACTATT	69801
OY	6110	tagctctctgagagcttcatttagattagttggtlccagaagttctgtgccctccatgtcag	6169
Db	69802	TAGCTCTCGAGAGCTTCAATTAGATTAGTGGTTGAGAGTTCTTGTGCCCCCTTCATGTGTAG	69861
RESULT	3		
LOCUS	AF007562	5300 bp DNA	PRI 18-MAR-1998
DEFINITION	Homo sapiens trabecular meshwork inducible glucocorticoid response protein (TIGR) gene, promoter region and partial mRNA sequence.		
ACCESSION	AF007562		
VERSION	AF007562.1	GI:2970123	
KEYWORDS	human.		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 5300)		
AUTHORS	Nguyen,T.D., Chen,P., Huang,W.D., Chen,H., Johnson,D. and Polansky,J.R.		
TITLE	Gene structure and properties of TIGR, an olfactomedin-related glycoprotein cloned from glucocorticoid-induced trabecular meshwork cells		
JOURNAL	J. Biol. Chem. 273 (11), 6341-6350 (1998)		
MEDLINE	98165818		
REFERENCE	2 (bases 1 to 5300)		
AUTHORS	Nguyen,T.D., Chen,P., Chen,H. and Polansky,J.R.		
TITLE	Direct Submission		
JOURNML	Submitted (10-JUN-1997) Ophthalmology, University of California San Francisco, 10 Kirkham Street, San Francisco, CA 94143-0730, USA		
FEATURES	Location/Qualifiers		
SOURCE	1..5300		
gene	/organism="Homo sapiens"		
	1..>5300		
	/db_xref="taxon:9606"		
promoter	/gene="TIGR"		
	1..5271		
mRNA	/gene="TIGR"		
	5272..>5300		
	/note="additional 3' sequence deposited as TIGR mRNA with GenBank Accession Number U85257"		
	/product="trabecular meshwork inducible glucocorticoid response protein"		

Dh 2041 TATTGAGTACTTATATCTGCCAGACACCAGACAAATAAGTGTGAGCAAAAGCATCTACTGC 2100
Oy 2210 cctaccctcgtggaggtgacagttctctcactgaaagcgtgagaaagaaatctaagacca 2160
Dh 2101 CCTACTCTGGGAGGTACAGATTCTCATGAGACGTGCAGAAATAATTAAGCCA 2160
Oy 2161 gccaaactaaacccagctgctgaaagaaagaaataaacacactctgaaagattgtgcg 2220
Dh 2161 GCCAACTTAACCCAGTCTGAAAGAAAGAAATAACACACTCTGAAGATTGTGGCC 2220
Oy 2221 agcatcccttaacaaagcaccctccctagcgccctcgtccctccatcgtgcccgaag 2280
Dh 2221 AGCATCCCTTAACAAGGCGACCTCCCTAGCGCCCTCTGCTCCATCGTGCCGGGAGG 2280
Oy 2281 ccccaagcccgagctctcacaagcctcctcctcactgaaagcgtgtgaagctggagct 2340
Dh 2281 CCCCCAACCCGAGCTTCCAAAGCTCCTCCCTCCATCACTCACAGCGTGCAGCTGGGCT 2340
Oy 2341 gctcgtctcccgtagatcgtctgtagatcgtgagctgagaccccttgctccagagct 2400
Dh 2341 GCCTCGCTCCCGTGAATCGTCTGTGCTGATCTGAGCTGAGACCTCTTGCTCCAGGCT 2400
Oy 2401 ccagaaagaaatgagagaggaagaaactagctaaaggaatctggaagaggaagtgcttc 2460
Dh 2401 CCAGAAAGAAATGAGAGGGAAGGAACTACTTAACGAGAAATCTGAGGCGGACAGTGTTC 2460
Oy 2461 ctccagagagaaaggggagctccacgtccagaggaattccaggaagtgaggagactgcaagag 2520
Dh 2461 CTCAGAGGAAAGGGGCTCCACGCTCCAGAGAAATCCAGAGGGGGGAGCTGCAGGGAG 2520
Oy 2521 tggggagcctggagcctgagcgggtgctgaaagcagagagggaggaagggagagctgaa 2580
Dh 2521 TGGGAGCCTGGGCGCTGAGCGGGTCTGAAGCGAGAAAGGTGAAGGCGCAAGGCTCAA 2580
Oy 2581 gctgcccagatgctcagtgctgctcaggggctggaggttctcgtctccctgctgagc 2640
Dh 2581 GCTGCCAGATGTTCAAGTGTTCACGGGGCTGGAGTTCCTTCCTTCCTGTGAGC 2640
Oy 2641 cttctacatcttctcctcgtcctggagagaaagactatacttcagaaaggaatgcaagcttc 2700
Dh 2641 CTTTATCTTTCTCTCTCTCTGAGAGAGAAAGTCTATTCTCATGAAGGATGCGATTTC 2700
Oy 2701 aataagtcagctgttaaaatctccaggggtgctgagtggttctcctcactcagaaagcccttat 2760
Dh 2701 ATAAAGTCAGCTGTAAATTCAGAGGTGTGCATGGTTCCTTCCTCACGAAAGCCCTTAT 2760
Oy 2761 ttaattggaaatataaggaagcagactcattccctgaagccgttaattcagagaaagtgac 2820
Dh 2761 TTAATGGGAATATAGGAAGCAGAGCTCATTTCTAGGCGGTTAATTCAAGGAAAGTGAC 2820
Oy 2821 tggagctcttctcctcactgacttctcgtgcaactaactgaagccctggtgagcttgacta 2880
Dh 2821 TGGAGTCTTTCTTTCTTCAATGTTCTTCTGGCAACTACTCAGCCCTGTGGTGACTTGCTTA 2880
Oy 2881 tgcagaagcgtctgaaaaacacttgaaatcagagagactcgttctcctcgtctgcttgcatt 2940
Dh 2881 TGCAAGAGCGTGAAGAACTCTTGAAATCAGAGACTCGGTTTCTTCTGATTCGCCATT 2940
Oy 2941 ggttggtcgtgagacgtgggcaagtgctctcctcctcctcgtggccatagtctctcgtc 3000
Dh 2941 GGTGTGGCTGTGCGACCGGGCAAGTGTCTCTCTTCCCTGGGCCATGTCTTCTCTGCT 3000
Oy 3001 aataagaccctctgagcctcgtgctgtctgtgaaacactcccttgatctctgtgaaaggg 3060
Dh 3001 ATAAAGACCTTGGAGCTCTGTGTCTGTGAACACTTCCCTGTGATTTCTGTGAGGGG 3060
Oy 3061 ggaatctgagagggagagagcagagctgagagcagctgagcccaagggagaggtggaggg 3120
Dh 3061 GGATCTTGAGAGGGGAAGAGAGAGAGCTGAGAGCTGAGACCAAGGGAGGTGAGAGG 3120
Oy 3121 ggaagagagagcagagcagagctggtgctcactcagctcctcactgatacagctcagactc 3180
Dh 3121 GGACAGGAAGCGCAGGCAAGAACTGGGTGCTCCATCAGTCTCACATGATCAGCTGAGACTC 3180

Oy 3181 caggaccgagaccacaatgcttcaggaagctcaatgaaacccacagccacatttctc 3240
Dh 3181 CAGAGCCGAGAGCCACATGCTTAGAGAAAGCTCAATGAACCCCAACGACCATTTTCT 3240
Oy 3241 tccctaagcatalagacaaatggcatcttgcaataaaccaaaaagaatgacagactaactcgt 3300
Dh 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATTAACCAAAAAGAAAGCAGAGACTAATCGT 3300
Oy 3301 ggttagctttggcctggcattcacaagaatlgggccagagcagtggaataatgcccagagt 3360
Dh 3301 GGTAGCTTTGGCTGGCATTTCAAAACTGGGCCAGACAAAGTGAATAATGCCAGATGTG 3360
Oy 3361 ttaaaccttcaacctgacagcccccacagcagctcagcagtgactcgtctgacagcag 3420
Dh 3361 TTAACCTTTTACCCCTGATCCAGCAACCCACAGCACTACGAGTACTGCTGACAGCAGG 3420
Oy 3421 agtgacctgacgagggagaggaagaaagagagggatagtgatagcagaag 3480
Dh 3421 AGTGACCTGACGCGCAGGGGAGAGAAAGAAAGAGGAGTATGTATGAGCAAGAAAG 3480
Oy 3481 acgaatcattcgaagcagtgaggaaatlgacccaaggaatatagttccagtgatccttg 3540
Dh 3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACACAGGGATTAATAGTCCAGTGTCTGG 3540
Oy 3541 gttcagaagcagggctataatg tgggggaaaaaaatcagttcaagggagtcggaga 3600
Dh 3541 GTTCTAGAGAGCAGCGCTATTTGTGGGGGAAATAATCAGTTCAAGGAAAGTGGGAGA 3600
Oy 3601 ccgtgattcctaatactatcttctccttaacagcgtgaaatctgagcaagtcacaag 3660
Dh 3601 CCTGATTTCTATCTATATTTTCTTACAGCTAGTAATCTCAGCAAGCACAGC 3660
Oy 3661 gtagtaactagaggtgtgaagatactagttctccctattaaggaactcttctcgt 3720
Dh 3661 GTAGTAACAGGCTGTAAGATTAAGTATGTTCTCTTATTAAGAACTCTTTCTGTG 3720
Oy 3721 ggaattagcagcaagggcaatccgcttcttcttaacaggaagaaacaatctcctaagag 3780
Dh 3721 GGATTTAGCAAGCAAGAGGCAATCCGTTCTTTAAGAGAAAGAAACATTTCTTAAGAG 3780
Oy 3781 taaagccaacaagatccaagcctagctcgtcgtgacataatgattggtcttctgaaaaat 3840
Dh 3781 TAAAGCCAAACAGATTCAGGCTTAGGCTTGACACTATATGATTTGTTTGAATAAT 3840
Oy 3841 cattcagagatggttactatctgattcagaaatlgagactagacccttggtcagctg 3900
Dh 3841 CATTTCAGCGATGTTACTATCTGATTCAGAAATGAGACTAGTACCCTTGGTCACTG 3900
Oy 3901 taaacaacaacccagctgttaaatgctcacaagtccaagcttaactgacagaaaccaaaaa 3960
Dh 3901 TAAACAACAACCCAGTGTAAATGTCTCAAGTTCAAGCTTAACGCAACCAATCAAA 3960
Oy 3961 agaatagaatcttaagagcaactggtcttctccacaatcggaggtgagctcgcagggc 4020
Dh 3961 AGAATAGAATCTTTAGAGCAAAAGTGTCTTCACATCTGGAGGTAGCTGCGCAGGC 4020
Oy 4021 agtttgaaatatattacttcaacaagtatlgacactggtgtgtgataaacaacaataagt 4080
Dh 4021 AGTTGGAATATTTACTTTCACAGATTAACACTGTTGTTGATTAACAACCTTAAGT 4080
Oy 4081 tgcataaaggcaatcattatctcagagtggtctaaagttaactctgacagtttggtaac 4140
Dh 4081 TGCCAAAGCAATCATTTATTTCAAGTGGCTTAAGTTACTTTCGACAGATTTGGTATAT 4140
Oy 4141 ttaatgcatatggcatttgcttcttctcctcctccttgggttataatgtaagcag 4200
Dh 4141 TTATTTGCTATTGCGCATTTGCTTTTGTCTTCTCTTGGGTTATTAATGTAAGACAG 4200
Oy 4201 ggaattataacctcagttccagaagagctgtgaattgaaatgggaaaaataactatctt 4260
Dh 4201 GGATTTAATCACTACAGTCCAGAAAGCTGTGAATTTGAATGAGGAAATAATTAATCATTTT 4260

4261 tgtttaccaccccttcaactaaattcaacatttattcattatgcagatagaccataaa 4320
4261 TGTTTTACCACCCCTTCAACTAAATTCAACATTTATTCCATTCGATAGACCATAAA 4320
4321 cccaaagtgttaataacagactctgtgacttctgcatltaaccaalagaatacagacatc 4380
4321 CTCAAAGTGTAAATAACAGTACTGTGATTTTGCATTACCAATGAAATCACAGACATT 4380
4381 ttatatactatctcaagtgctgttcagataagctgtgaagtgaataattatataccta 4440
4381 TTATATCTATATTCAGTGTGTGAGATACGTTGAACTGAAATATTTATCTCAAACTA 4440
4441 ctctgaataatlagacctccctcgtgactctgttcttaacatactaaataacatcttaaa 4500
4441 CTCTGAATAATLAGACCTCCTCGTGATCTGTGTTTAAATATTAATAACATTTTAAA 4500
4501 attctgatacttgaataacatattcattatcaattctgttcccttcttaacatacttc 4560
4501 ATTTTGATATTTGATATCATATTTATCATATTTGTTTCCCTTTGTAATCTATATTTT 4560
4561 atatatctgaataacatctctcgaagaaggtccccaagattcccaatgaggtctctg 4620
4561 ATATATTTGAAACATATTTCTGAGAAAGTTCCCGAGATTTCACCAATGAGGTCTTGG 4620
4621 catgcacacacacagagtaagaactgaattagaagctaacatgacattggtgctgaga 4680
4621 CATGCAACACACAGACTAGAACTGATTTAGAGGCTTAACATTGAGTGGCTGAGA 4680
4681 tgcagaagctgaataatagaagctctcccaagaatatacagaagttgttcttaagaagctg 4740
4681 TGCAGAGCTGAATAATAGAAAGTTCTCCCAAGATACAGATTGTTTAAAGCTAGGGGTG 4740
4741 agggggggaatactgcgcctcttaagaagaagctccctcgaagaagctgtgaaggtctg 4800
4741 AGGGGGGAAATCTGCCCTCTTATAGAAAGCTCTCCCTGAGGCTGTGAGGTGCTGTC 4800
4801 ctgtgctcgtcgtcgtcgttatttctcctcgtcctcgtcctcgtcctaaagaagcttct 4860
4801 CTGTGCTTCTGCGCTGCTGTTATTTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4860
4861 ggaatccagatccctagacataagctcgtgcagagtgcaaggtctcgaatgagttgcagag 4920
4861 GGATCTCCAGTCTCTACATAGTCCCTGCGCACAGTGCAGGTTCTCAATGAGTTTGCAGAG 4920
4921 tgaatgaataataactagaataataatccctgttgaataatcagacacccagtaactctg 4980
4921 TGAATGGAATAATAACTAGAAATATATCTTGTGAATCAGACACACAGTACTCTCTGG 4980
4981 tgaagctgtctgaagctgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 5040
4981 TGTAACTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5040
5041 taagaactatatttgggtgagtgatgagtaaaattgggaatgttcttcttaaaagaatctc 5100
5041 TAGAACTATATATGGGCTAGGCTGATTAATGGGATGTTCTTTTAAAAAAGAAATCTC 5100
5101 caaaacaaactcttgaaaggtatatttcttaagaatactcgtcgtgcagcgtgaaagaaacccc 5160
5101 CAAACAAACTCTTGGAAGGTATTTTCTTAAGAATCTTGCTGCGAGCGGAGGGAACCC 5160
5161 cctgtgacagagcccaacacagcctcaagctgtgcacacccctcctccccaagaaaggtctg 5220
5161 CCTGTGACAGAGCCCAACAGCTCAGCTGCGACCTCTGCTTCCCCCAAGAAAGGCTG 5220
5221 gctcccaagatataataaacctctcgtgaagctcgggcaatgaagccagaaagcccaatc 5280
5221 GCTCCCAAGATATATAAACCTCTGTGAGCTCGGCGATGAGCAGCAAGCCACCATC 5280
5281 caggacacctctcagcagcagc 5300
5281 CAGGACCTCTCAGCAGCAGC 5300

RESULT 4
LOCUS HSMYOC1 2800 bp DNA PRI 21-APR-1998
DEFINITION Homo sapiens myocilin (GLC1A) gene, promoter and exon 1.
ACCESSION AF049791
VERSION AF049791.1 GI:3065670
KEYWORDS 1 of 3
SEGMENT 1
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 2800)
AUTHORS Finger, J.H., Ying, L., Swiderski, R.E., Nystuen, A.M., Arbour, N.C.,
Alward, W.L.M., Sheffield, V.C. and Stone, E.M.
TITLE Characterization and comparison of the human and mouse GLC1A
glaucoma genes
JOURNAL Genome Res. (1998) In press
REFERENCE 2 (bases 1 to 2800)
AUTHORS Finger, J.H., Ying, L., Swiderski, R.E., Nystuen, A.M., Arbour, N.C.,
Alward, W.L.M., Sheffield, V.C. and Stone, E.M.
TITLE Direct Submission
JOURNAL Submitted (23-FEB-1998) Ophthalmology, University of Iowa, 200
Hawkins Drive, Iowa City, IA 52242, USA
FEATURES
source
1..2800
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1q21-q31"
1..1905
/gene="GLC1A"
1905..2809
/gene="GLC1A"
/number=1
BASE COUNT 781 a 588 c 673 g 758 t
ORIGIN
Query Match 43.4%; Score 2677.4; DB 66; Length 2800;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2736; Conservative 0; Mismatches 1; Indels 8; Gaps 5;
QY 3431 agcgaaggagaggaagaagaagaagaagatgtagtgcagaaagaacagatcat 3490
DB 1 AGCCGAGGAGGAGGAAG-AAAAGAGAGGATAGTGTATAGCAAGAAACAGATTGAT 59
QY 3491 tcaaggcagctgggaattgacacagagattatagtcacagtgatccctgggttcaggag 3550
DB 60 TCAAGGCGACGTGGGAATTGACACAGAGGATTATAGTCACGATGATCCTGGGTCTAGAG 119
QY 3551 gcaggcctaatctgtggggggaataatcagctcgaagggaagtcgggaagcctgattct 3610
DB 120 GCAGGCTATATGTGGGGGGAATAATCAAGTCAAGGGAAGTCGGAGACCTGATTCT 179
QY 3611 aatactatatttcccttcaagctgagtaattctgagcaagtcacaaagtagtaactg 3670
DB 180 AATACGTATATTTTCTTCAAGCTGAGTAATTTCTGAGCAAGTACAGAGTAACTG 239
QY 3671 aggcgtgaagattactagttcttcccttattagaaactcttctctctgtggaattagca 3730
DB 240 AGCGTGAAGATTACTAGTTCCTTCTTATTAGAACTCTTTTCTGCTGTGAGATTGCA 289
QY 3731 gcacaaggcgaatccgcttcttcaagagaagaataacttccctaagtaagccaata 3790
DB 300 GCACAAAGGCAATCCCTTTCTTTTAAAGAAAGAAACATTTCTTAAGATTAAGCCAAA 359
QY 3791 cagatcaagcctagagctcgtcgtacataatgattgtttcttgaagaatacatcttcagcg 3850
DB 360 CAGATTAAAGCTTAGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 419
QY 3851 atgttactactgattcagaagaatgagactagtaacccttctgtcagctgttaacaaaca 3910

Dh	420	ATGTTTACTATCGATTCCAGAAATATGAGACTAGTACCCTTTGGTCAAGCTGTAAACAACA	473
Oy	3911	CCcagcttgtaaaatgctcacaagtctcagaagctbaactgcagaaaccaatcaaa-aagaaataga	39659
Dh	480	CCCATTTGTAAATGTCTCAAGTTCAGGCTTAAGTCCAGAACCAATCAATAATAGAAATAGA	539
Oy	3970	tcttttagagcaaaactggtcttcccaactctggaagtgtgtctgcacgggcagctttgaa	4029
Dh	540	TCTTTAGGCAAACTGTGTTCTCCAC-TCTGGAGGTGAGTGTGCAGGGCAGTTTGGAA	598
Oy	4030	aatttaactcaacaagatctgacaacgtctgtgtga tcaacaacaataagttctcaag	4089
Dh	559	ATATTACTTACAAAGATATTGACACGTCTTGTGATTAACACATTAAGTTGCTCAAG	658
Oy	4090	gcaalcacatlttcaagctggccttaaaagttlaactctgcacagctttgtaabattatlgct	4149
Dh	659	GCAATCATTAATTTCAAGTGGCTTAAGTTACTTCTGACAGTTTGGTATATTAATGAGCT	718
Oy	4150	attgcacattgcttcttctgttcttcccttgggttcaataatgtaaagcaggattatla	4209
Dh	719	ATTGCAATTGCTTTTGTGTTTCTCTTGGGTTTATTAATGAAGCAGGATTAATA	778
Oy	4210	accctacgttccagaagcccgctgaacttgaatgaaggaaaaaattacattttgttttac	4269
Dh	779	ACCTACAGTCCAGAAACCTGTGAATTTGAATGAAATGAGAAAAATTACATTTTGTTTTAC	838
Oy	4270	caccttccaaactaaattcaacattctcaactctggaatagaagccataaactcaaaag	4339
Dh	839	CACCTGTCACTAAATTAATTAACATTTTATTCATTTGGAATAGGCAATTAAGTCAAACTG	898
Oy	4330	gtaabaacagtaacctgtgattctgtcaatcaaatgaatacaagacaattatlaactat	4389
Dh	899	GTAATACAGACTGCTGATTTTGCTATTGCCAATGAAGATCACAGACATTTATATCAT	958
Oy	4390	attcaagttgtgtgaagtaaggttgaaagtgaatattctactcaaaactactttgaat	4449
Dh	959	ATTACAGTTGTTGGAGATACGCTGTGAAGTGAATTAATTAATTAATTAATTAATTAAT	1018
Oy	4450	tagaccctccctcgtgaactcgttcttaacaataaataaacaatgctttaaactttgta	4509
Dh	1019	TAGACCTCTCTGCTGATCTTGTTTAACTATTAATTAACATGTTTAAATTTTGATA	1078
Oy	4510	tcttgataatcatatltcaatlaacttgttcttcccttggtaactatattatlaacttg	4569
Dh	1079	TTTGTGATATCATATTTCATTATCATTTGTTGCTTTGAATCACTAATTTTATATATYG	1138
Oy	4570	aaaacactctctgaagaaggtctcccaagattccaccaatggagtctctggaatgcaac	4629
Dh	1139	AAAACATCTTCTGAGAAAGTTCCCCAGATTTCCACCAATGAGGTTCTTGCGATCCAC	1198
Oy	4630	acacagagtaagaactcgaattctagaagcttaacatctgaactgtgtcctggaatgcaagct	4689
Dh	1199	ACACAGAGTAAAGACTATTTAGAGGCTTAACATTTGATTTGCTGCTGAGATGCAAGCT	1258
Oy	4690	gaaatagaagaagcttcccaagaatacacagttgtttaaagctgaagggtctgaaggga	4749
Dh	1259	GAATTAAGAAAGTCTCCCAAGATACAGAGTGTTTAAAGCTAGGGGTGAGGGGGAA	1318
Oy	4750	actgcgcgtctctatagaatgtcctccctcctggaagcctgtgtaggtgtgtcctgtgttc	4809
Dh	1319	ATTCGCCGCTCTATAGGAATGCTCTCCCGAGAGCTGTGATAGGAGTCTCTTGTGTTC	1378
Oy	4810	tgtcgtgctgttatttcttctctgtccctgtcgaagctttaaaggaacttgttggatctcca	4869
Dh	1379	TGGCTGGCTGTATTATTTTCTGTGCTCTGCTAGCTTTAAAGACTGTGTTGGATCTCCA	1438
Oy	4870	gttctctagaacagcctctggaagcgtcgaagttctcaatgagttctgcaagatgaaataga	4929
Dh	1439	GTTCTTACATAGTGGCTGTGGACAGTGCAGAGTCTTAATGAGTTTGCAAGAGTAATGAA	1498
Oy	4930	atacaaaactagaataatacactctgtgtgaatacgaacacacagtaagctcctgtgtgaagt	4989
Dh	1499	ATATTAAGCTAGAAATATATCTCTTGTGAAATGACACACAGTAAAGTCTGTGATAGCT	1558

[illegible]

Oy	6066	aattagaagaacacac-gatcacccctcaagatctactagtaattagctcccgagagct	6124
Oy	6125	tcattagaattagtggttcagaagttcttgccctccatcgaatgcag	6169
Oy	6269	tcatttagattagtggttcagagttcttgccctccatcgaatgcag	2743
Db	2639	aatTAAGCAAAACACAGCAGCATCACCCTTCAAGATATTCTAGTAATTAGCTCCGAGAGCT	2698
RESULT	5		
LOCUS	AB006686S1		
DEFINITION	AB006686S1	1228 bp	DNA
ACCESSION	AB006686S1		PRI
VERSION	AB006686.1	GI:2828342	14-APR-2000
KEYWORDS	myocilin.		
SEGMENT	1 of 3		
SOURCE	Homo sapiens pre-pro-B cell cell_line:FLNB14-14 DNA, clone_11b:BAC clone_KB780C12.		
ORGANISM	Homo sapiens		
REFERENCE	1 (sites)		
AUTHORS	Escribano, J., Ortego, J. and Coca-Prados, M.		
TITLE	Isolation and characterization of cell-specific cDNA clones from a subtractive library of the ocular ciliary body of a single normal human donor: transcription and synthesis of plasma proteins		
JOURNAL	J. Blochem.	118 (5),	921-931 (1995)
MEDLINE	96318503		
REFERENCE	2 (sites)		
AUTHORS	Stone, E.M., Fingert, J.H., Alward, W.L., Nguyen, T.D., Polansky, J.R., Stenden, S.L., Nishimura, D., Clark, A.F., Nyström, A., Nichols, B.E., Ritch, R., Kalenak, J.W., Craven, E.R. and Sheffield, V.C.		
TITLE	Identification of a gene that causes primary open angle glaucoma		
JOURNAL	Science	275 (5300),	668-670 (1997)
MEDLINE	97158493		
REFERENCE	3 (sites)		
AUTHORS	Kubota, R., Noda, S., Wang, Y., Minoshima, S., Asakawa, S., Kudoh, J., Mashima, Y., Oguchi, Y. and Shimizu, N.		
TITLE	A novel myosin-like protein (myocilin) expressed in the connecting cilium of the photoreceptor: molecular cloning, tissue expression, and chromosomal mapping		
JOURNAL	Genomics	41 (3),	360-369 (1997)
MEDLINE	97312692		
REFERENCE	4 (sites)		
AUTHORS	Kubota, R., Kudoh, J., Mashima, Y., Asakawa, S., Minoshima, S., Hejtmancik, J.F., Oguchi, Y. and Shimizu, N.		
TITLE	Genomic organization of the human myocilin gene (MYOC) responsible for primary open angle glaucoma (GLCIA)		
JOURNAL	Biochem. Biophys. Res. Commun.	242 (2),	396-400 (1998)
MEDLINE	98113364		
REFERENCE	5 (bases 1 to 1228)		
AUTHORS	Shimizu, N. and Kudoh, J.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-AUG-1997)		
MEDLINE	Submitted (16-AUG-1997)		
REFERENCE	Nobuyoshi Shimizu, Keio University School of Medicine, Department of Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo 160-8582 Japan (E-mail:shimizu@med.keio.ac.jp, Tel:81-3-3351-2370(ex.2720), Fax:81-3-3351-2370)		
AUTHORS	Location/Qualifiers		
TITLE	1..1228		
JOURNAL	/organism="Homo sapiens"		
MEDLINE	/db_xref="taxon:9606"		
REFERENCE	/cell_line="FLNB14-14"		
AUTHORS	/cell_type="pre-pro-B cell"		
TITLE	/chromosome="1"		
JOURNAL	/clone="KB780C12"		
MEDLINE	/clone_11b="BAC"		
REFERENCE	/map="1q23-q24"		
AUTHORS	16..221		
TITLE	/note="glucocorticoid responsive element consensus sequence"		
JOURNAL	371..375		
MEDLINE	TATA-signal		

[illegible]

Db	899	CAGAACCTCTCTCCGAGACAAAGTCAGTTCTGGAGGAAAGAGAAACGACCTAAGCGAAGA	958
Qy	5822	AAATggaatcttggccagagaggtttggaagacagccagagaggtatgcaagcttgaag	5881
Db	959	AAATGGAATCTTGCCCGAGGAGTTTGAAGAACACACACCAGAGATGTGCAAGCTTGAAG	1018
Qy	5882	gggcagatgtccccagagaccgagacactgtctcgagctgttaccacagagctccagagaag	5941
Db	1019	GGGCGATGTCTCCAGACCCGAGACACTGCTCGGGCTGTGCCACAGGCTCCAGAGAAAG	1078
Qy	5942	taagaatgycagagttgggggaattctgaagtcagacaggtgatatgctctgaatgacctgc	6001
Db	1079	TAAAGATGCAAGAGGGGGGACACTGTGATGTTACACAGGTGATTAAGGCTCTGATGACCTTC	1138
Qy	6002	tacagcgctccagagcctc-----cctgcaccttctcctatagaagactcagacatlagacaa	6057
Db	1139	TACAGCGGCTCCAGGCTCTCCCTGCTGCCCTTTCTCTTACAGACTCCACAGGTAGACAA	1198
Qy	6058	gacacgatgatatgaaggaagacaca	6081
Db	1199	GACAGATGAATTTAAGGAAGCAC	1222

RESULT	6
LOCUS	HSGCLC1A 1086 bp DNA PRI 30-JAN-1998
DEFINITION	Human septans GLCIA (irabascular meshwork induced glucocorticoid response) gene, exon I, joined CDS.
ACCESSION	297171
VERSION	297171.1 GI:2425156
SOURCE	GLCIA.
ORGANISM	human.
REFERENCE	Human septans
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 1086) Stone,E.M., Flinder,J.H., Alward,W.L., Nguyen,T.D., Polasky,J.R., Sundén,S.L., Nishimura,D., Clark,A.F., Nyström,A., Nichols,B.E., Ritch,R., Kalenak,J.W., Craven,E.R. and Sheffield,V.C. Identification of a gene that causes primary open angle glaucoma Science 275 (5300), 668-670 (1997) 97158493 2 (bases 1 to 1086) Adam,M.F., Belnouën,A., Binisti,P., Brezin,A.P., Vaitot,F., Becheuille,A., Descotte,J.C., Copin,B., Gomez,L., Chaventre,A., Bach,J.F. and Garchon,H.J. Recurrent mutations in a single exon encoding the evolutionarily conserved glactomedin-homology domain of RGR in familial open-angle glaucoma Hum. Mol. genet. 6 (12), 2051-2097 (1997) 97472461 3 (bases 1 to 1086) Garchon,H.J. Direct Submission Submitted (20-JUN-1997) Garchon H.-J., Hopital Necker, INSERM U25 161 rue de Sevres 75743 Paris cedex 15 FRANCE location/Qualifiers
FEATURES	source
	1..1086
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/chromosome="1"
	/map="q23-q25"
	/tissue-type="white blood cells"
	355..363
TATA_signal	385..1065
exon	/gene="GLCIA"
	/label=ex1
	/number=1
mRNA	join(385..1065,297177.1:21..146,297174.1:21..1475)
	/gene="GLCIA"
	/label=RNAGLAIA
gene	join(385..1065,297177.1:21..146,297174.1:21..1475)
	/gene="GLCIA"

[illegible]

```

|||||
Db 661 CCATGTCAGTCATCCATTAAGACAGAGACAGACAGACCCCAACGCTTAGACCTGAGAG 720
OY 5596 ccaacaaagctgactcaactcctctgagaagctcctcctcaacaaatgactctgaccagg 5555
Db 721 CCACCAAACTGACACACACTCCCTGAGAGCTCCTCCACCAATTGACCTTGAGACAG 780
OY 5656 cgcacagagcccccagagagaccccaagaggcctgacagaggagcctgagccctcaaggcgg 5715
Db 781 CTGCCAGGCCCCAGAGACCCAGAGAGGGCTGCAAGAGGAGCTGGCCACCTTAGAGCGGG 840
OY 5716 agcgggagacagctgagaaacccaacagagagcttgagagactgctcaacagaaactctcc 5775
Db 841 AGCGGAGACAGCTGGAACCAACCAACAGAGAGTTGGAGACTGCTACAGAACCTCTCC 900
OY 5776 gagacaagtcagctctcgaggagaaagaaagcgcactaaagcaagaataatgaaatctgg 5835
Db 901 GAGACAACTCAGTCTTGAGGAGAGAGAGAGAGAGCTAAGGCAAGAAATGAGAAATCTGG 960
OY 5836 ccagagagcttgagaaagcagcagcagagagctagcaagagcttgagaaagggcagctgcccc 5895
Db 961 CCAGAGAGTTGGAACACAGCAGCAGAGAGGTACCAAGGCTGAGAGAGGGCCAGTGTCCC 1020
OY 5896 agaccgagacacactgctcgaggctgctgccaacagagctcagagaaaggtaagaatgcagagt 5955
Db 1021 AGACCCGAGACACTGCTCGGGCTGTGCAACAGAGCTCCAGAGAAAGTAAGCAATGACAGAT 1080
OY 5956 gggggg 5961
Db 1081 GGGGGG 1086

RESULT 7
LOCUS D88214 1934 bp mRNA PRI 07-FEB-1999
DEFINITION Homo sapiens mRNA for myocillin, complete cds.
ACCESSION D88214
VERSION D88214.1 GI:2627176
KEYWORDS myocillin.
SOURCE Homo sapiens retina cDNA to mRNA, clone_11b:human retina cDNA
LIBRARY 5' stretch (CONTECH).
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 1934)
AUTHORS Shimizu,N.
TITLE Direct Submision
JOURNAL Submitted (02-OCT-1996) to the DDBJ/EMBL/GenBank databases.
Nobuyoshi Shimizu, Keio University School of Medicine, Department
of Molecular Biology, 35 Shinanomachi, Shinjuku-ku, Tokyo 160,
Japan (E-mail:shimizu@dm.med.keio.ac.jp, Tel:03-3351-2370,
Fax:03-3351-2370)
2 (sites)
REFERENCE 2 (sites)
AUTHORS Kubota,R., Noda,S., Wang,Y., Minoshima,S., Asakawa,S., Kudoh,J.,
Mashima,Y., Oguchi,Y. and Shimizu,N.
TITLE A novel myosin-like protein (myocillin) expressed in the connecting
cilium of the photoreceptor: molecular cloning, tissue expression,
and chromosomal mapping
JOURNAL Genomics 41 (3), 360-369 (1997)
MEDLINE 97312692
COMMENT On Nov 20, 1997 this sequence version replaced gi:2104213.
FEATURES
Location/Qualifiers
1..1934
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/clone_11b="human retina cDNA library 5' stretch (CONTECH)"
/map="1q23-q24"
/tissue_type="retina"
65..1579
/codon_start=1
/product="myocillin"

```

```

/protein_id="BAA23531.1"
/db_xref="GI:2627177"
/translation="MRFECARCCSFGEPMFAPVOLLACIYWDVGARTAOLRKANDOS
GRQYTESVASPNESSECEPOSOAMVITNLRDSTQQLDLEATARSLSELSLHOL
TLDDARQETQEGQLRELTREDDLETRLETAYSNLNDKSVLEEKRLR
QENENLARLESSQEVARLRGQDPOIRDRAVAPSPSREVTNNLDTLAEOLKSE
LTENPASRLKESPGLRSGEGDCEELVWVGEPILRLTAEITTGXGVWRDPPK
TYPYQERTMRIDVTGTVROYFEXDLISQFMOGYPSKVIILPRLSESTGAVYSGSL
YFOGASRTVIARYELNTEFVKAERKILPGAGYHGOFRPMGGCTDIDLAVDEAGLWVI
STDEAKGAIIVSLKLPENLEBOTETETINIKROSVANATLICGTLTVTSYTSADTVN
FAYDTGISIKTLTILPFKNRYISMDINPLEKRLFAMDNLNMTYDIKISKM"
old_sequence
104..105
/citation={2}
/replace="gaga"
misc_feature
317..361
/note="leucine zipper-like motif 1"
misc_feature
413..562
/note="leucine zipper-like motif 2"
polya_signal
1778..1783
polya_signal
1928..1933
BASE COUNT 510 a 503 c 525 g 396 t
ORIGIN
Query Match 10.6%; Score 651.2; DB 35; Length 1934;
Best local Similarity 99.5%; Pred. No. 5.4e-132;
Matches 653; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 5287 cctctcagaacagcagaagctcttcagaagaaagcctcacaagcctctgcaatgagttct 5346
Db 15 CCCTCTGCAACAGACAGAGCTTTCAGAGAGAGCTCACCAGGCTCTGCAATGAGTTCT 74
OY 5347 tctgtcacgtgtctgcaacttgggcctgagagatgacagctgcagcagctgctctctg 5406
Db 75 TCTGTGACAGTTGCTGCAAGCTTTGGCTGAGATGCCAGCTGTCCAGTCTGCTCTG 134
OY 5407 cctgcctgtgtgtggaatgttgggggccaagcagcctcagctcagagaaagcacaatgacaga 5466
Db 135 CCGTGGCTGGTGTGGAGTGTGGGGCCAGGACAGCTCAGCTCAGAGAGGCCAATGACAGA 194
OY 5467 gtggccgagtcagatgacctgagctgagtcagctcccaatgaaatccagctgccagagc 5526
Db 195 GTGGCCGATGCCAGTATACCTTCAGTGTGGCCAGTCCCAATGATACCTGCCAGAGC 254
OY 5527 agagcagagccatgtaagcatcacaacttacaagagaacacacacacacgcttag 5586
Db 255 AGAGCCAGGCGCATGTATCATTAATTAACAGAGAGACAGACACACACGCTTAG 314
OY 5587 accctgagccacacaaagctcgaactcagctccctctgagagagcctcctcccaatgacct 5646
Db 315 ACCTGGAGCGCACCAAGCTCGACTCCCTGGAGAGCTCTCCACCAATTGACCT 374
OY 5647 tggacagagctgcagagcccccagagaaacccaagaggctgcagagaggctgggacccc 5706
Db 375 TGGACCAAGCTGTCACAGGCCCCACAGAGAGAGGAGGCTGAGAGGAGCTGGCACCC 434
OY 5707 tggaggggagagggagcagctggaaccccaacccaagagtggtggagctgcttacaaga 5766
Db 435 TGAAGCGGGAGCGGAGCACAGCTGGAAACCAACAGAGAGTTGGAGCTGCTTACAGCA 494
OY 5767 accctctcagaagaagtcagctctgagagaaagagaagcgaactcaagcacaagaatg 5826
Db 495 ACCTCTCGAGACAGTCACTTCTGAGAGAAAGAGAACGACCTRAAGCAAGAAATG 554
OY 5827 aagaatcgacagagagcttgaaagacagcagcagaggtgagcaagctgagaagggcc 5886
Db 555 AGAATCTGGCCAGAGAGAGTTGGAAGCAGCAGCCAGAGAGTAAAGCTGAGAAAGGGGCC 614
OY 5887 aggtgtcccccagaccagacagctcgaggctgtgccaacagagctccaagaagaggt 5942
Db 615 AGTGTCCCGACAGCCGAGACACTGTGGGCTGTGACACACAGGCTCCAGAGAGATT 670

```

RESULT 8
LOCUS AR030962 1999 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5861497.
ACCESSION AR030962
VERSION AR030962.1 GI:5944176
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1999)
AUTHORS Nguyen,T.D., Polansky,J.R. and Huang,W.
TITLE Triebecular meshwork induced glucocorticoid response (TIGR) nucleic acid molecules
JOURNAL Patent: US 5861497-A 2 19-JAN-1999;
FEATURES Location/Qualifiers
source 1..1999
BASE COUNT 537 a 508 c 534 g 420 t
ORIGIN

Query Match 10.4%: Score 640.4; DB 5; Length 1999;
Best Local Similarity 99.8%; Pred. No. 1.2e-129;
Matches 641; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 5301 agagcttcacagaggaagccctcaccaagcctctgcaatgaggtctctctgacagctgac 5360
|||||
Db 1 agagctttccacagaggaagccctcaccaagcctctgcaatgaggtctctctgacagcttgc 60
|||||

Oy 5361 tgcagctctgggcccgtgagatgccaagctgctcagctgctctctgctgctgctgctgctg 5420
Db 61 tgcacctttgggcccgtgagatgccaagctgctcagctgctctgctgctgctgctgctgctg 120
|||||

Oy 5421 gatgryggggccagagacagctcagctcagagaaagccaatgacagagatgagcagatgacag 5480
Db 121 gatgryggggccagagacagctcagctcagagaaagccaatgacagagatgagcagatgacag 180
|||||

Oy 5481 tataccttcagatgctggccagctcccaatgacagctgcccagagacagagccagatg 5540
Db 181 tataccttcagatgctggccagctcccaatgacagctgcccagagacagagccagatg 240
|||||

Oy 5541 tcagctcattcaacttcaacagagagacagcagaccaccaagcttagaaccttgagggccaac 5600
Db 241 tcagctcattcaacttcaacagagagacagcagaccaccaagcttagaaccttgagggccaac 300
|||||

Oy 5601 aaagctcgaactcagctccctctgagagagcctcctcccaattgaccttgagcagagctgac 5660
Db 301 aaagctcgaactcagctccctctgagagagcctcctcccaattgaccttgagcagagctgac 360
|||||

Oy 5661 agggcccccagagagacccagagagggctgacagagagctggagccctggagggagcag 5720
Db 361 agggcccccagagagacccagagagggctgacagagagctggagccctggagggagcag 420
|||||

Oy 5721 gaccagctggaaccccaaacagagagatgtgagagctgctcactacagaaacctcctccgagac 5780
Db 421 gaccagctggaaccccaaacagagagatgtgagagctgctcactacagaaacctcctccgagac 480
|||||

Oy 5781 aagtcagctctgagagagagagagagagcagcctaagggcaagaaatgagaaatctggccag 5840
Db 481 aagtcagctctgagagagagagagagagcagcctaagggcaagaaatgagaaatctggccag 540
|||||

Oy 5841 aggttggaaaagcagcagcagagagatgacaaagctgagaaagggcagctgtccccaagacc 5900
Db 541 aggttggaaaagcagcagcagagagatgacaaagctgagaaagggcagctgtccccaagacc 600
|||||

Oy 5901 cgaagacactgctcgggctgtgcccacagagctccagagaagt 5942
Db 601 cgaagacactgctcgggctgtgcccacagagctccagagaagt 642
|||||

RESULT 9
AR066022

LOCUS AR066022 1999 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5849879.
ACCESSION AR066022
VERSION AR066022.1 GI:596238
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1999)
AUTHORS Nguyen,T.D., Polansky,J.R. and Huang,W.
TITLE Methods for the diagnosis of glaucoma
JOURNAL Patent: US 5849879-A 2 15-DEC-1998;
FEATURES Location/Qualifiers
source 1..1999
BASE COUNT 537 a 508 c 534 g 420 t
ORIGIN

Query Match 10.4%: Score 640.4; DB 5; Length 1999;
Best Local Similarity 99.8%; Pred. No. 1.2e-129;
Matches 641; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 5301 agagcttcacagaggaagccctcaccaagcctctgcaatgaggtctctctgacagctgac 5360
|||||
Db 1 agagctttccacagaggaagccctcaccaagcctctgcaatgaggtctctctgacagcttgc 60
|||||

Oy 5361 tgcagctctgggcccgtgagatgccaagctgctcagctgctctctgctgctgctgctgctg 5420
Db 61 tgcacctttgggcccgtgagatgccaagctgctcagctgctctgctgctgctgctgctgctg 120
|||||

Oy 5421 gatgryggggccagagacagctcagctcagagaaagccaatgacagagatgagcagatgacag 5480
Db 121 gatgryggggccagagacagctcagctcagagaaagccaatgacagagatgagcagatgacag 180
|||||

Oy 5481 tataccttcagatgctggccagctcccaatgacagctgcccagagacagagccagatg 5540
Db 181 tataccttcagatgctggccagctcccaatgacagctgcccagagacagagccagatg 240
|||||

Oy 5541 tcagctcattcaacttcaacagagagacagcagaccaccaagcttagaaccttgagggccaac 5600
Db 241 tcagctcattcaacttcaacagagagacagcagaccaccaagcttagaaccttgagggccaac 300
|||||

Oy 5601 aaagctcgaactcagctccctctgagagagcctcctcccaattgaccttgagcagagctgac 5660
Db 301 aaagctcgaactcagctccctctgagagagcctcctcccaattgaccttgagcagagctgac 360
|||||

Oy 5661 agggcccccagagagacccagagagggctgacagagagctggagccctggagggagcag 5720
Db 361 agggcccccagagagacccagagagggctgacagagagctggagccctggagggagcag 420
|||||

Oy 5721 gaccagctggaaccccaaacagagagatgtgagagctgctcactacagaaacctcctccgagac 5780
Db 421 gaccagctggaaccccaaacagagagatgtgagagctgctcactacagaaacctcctccgagac 480
|||||

Oy 5781 aagtcagctctgagagagagagagagagcagcctaagggcaagaaatgagaaatctggccag 5840
Db 481 aagtcagctctgagagagagagagagagcagcctaagggcaagaaatgagaaatctggccag 540
|||||

Oy 5841 aggttggaaaagcagcagcagagagatgacaaagctgagaaagggcagctgtccccaagacc 5900
Db 541 aggttggaaaagcagcagcagagagatgacaaagctgagaaagggcagctgtccccaagacc 600
|||||

Oy 5901 cgaagacactgctcgggctgtgcccacagagctccagagaagt 5942
Db 601 cgaagacactgctcgggctgtgcccacagagctccagagaagt 642
|||||

RESULT 10
AR069089
LOCUS AR069089 1999 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5854415.
ACCESSION AR069089

VERSION AR069089.1 GI:6001296
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1999)
AUTHORS Nguyen,T.D., Polansky,J.R. and Huang,W.
TITLE Methods for the diagnosis of glaucoma
JOURNAL Patent: US 5854415-A 2 29-DEC-1998;
FEATURES Location/Qualifiers
source 1..1999
BASE COUNT 537 a 508 c 534 g 420 t
ORIGIN

Query Match 10.4%; Score 640.4; DB 5; Length 1999;
Best Local Similarity 99.8%; Pred. No. 1,2e-129;
Matches 641; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

5301 aaagcttccagaggaagcctcaccaagcctcgaatgagttctctgtgacgttcg 5360
|||||
1 AGAGCTTTCACAGAGAACCTCACAGCCTCTGCATGAGTTCTTGTGCACGTTGC 60
5361 tgcagccttgagcctgagatgcagcctgtccagctgtctctcgtgagcgtgtg 5420
|||||
61 TGCAGCTTTGGGCTTGAGATGCCAGCTGTCCAGCTCTGCTTGTGGCTGCTGTTGG 120
5421 gatttgaggagcagagacagctcagctcaggaagggccaatgacagagatggccag 5480
|||||
121 GATGTGGGGGCCAGAGACACTCAGCTCAGAGAAAGCCAAATGACAGAGATGGCCATGCCAG 180
5481 tctactctcagtggtgagcagctcccaatgatactcagctgtcccaagagagagccagagc 5540
|||||
181 TATACCTTCAAGTGTGGCCAGCTCCCAATGAATCCAGTGGCCCAAGAGAGCCAGGCCATG 240
5541 tcaatcatcataactctacagagagacagcagcagcagcagccttaagccttgagagccacc 5600
|||||
241 TCAGTATCATCAACTTACAGAGAGACAGACAGCCCAACGCTTAACCTCGAGGCCACC 300
5601 aaagctcgaactcagctcccttgagagagcctcctccacaaattgaaccttgagcagagctgcc 5660
|||||
301 AAAGCTCGACAGCTCCTCGAGAGCTCCTCCACCAATGACCTTGGACACAGCTGCC 360
5661 aagccccagagagacccagagagggctgcagagagagagctggccacctgagggcgagagcg 5720
|||||
361 AGGCCCCAGAGAGCCAGAGGGGCTGCAGAGGAGACTGGGCACTCTGAGGCGGAGCGG 420
5721 gaccagctgaaacccaacccagagaggttggaagactgctctacagcaacctcctccgagagc 5780
|||||
421 GACCACTTGAAACCCAAACCAAGAGATTGGAGACTGCTTACAGCAACCTCCTCCGAGAC 480
5781 aagtcagctctgagagagagagagagcgaactaaggcaagaaatgagaattcgccagag 5840
|||||
481 AAGTCAGTCTTGAGAGAGAGAGAGCGACGACCTAAGGCAAGAAATGAGAAATCTGGCCAGG 540
5841 aggtctgagaaagcagcagcagagaggttagcaaggtctgagaaggggccaagtgctcccgacc 5900
|||||
541 AGCTTGGAAGAGCAGCAGCAGAGAGGTAGCAAGGCTAGAAAGGGGCCAGTGTCCCGAGACC 600
5901 cgaagacagctcgtggagctgtgacacagaggtctcagagaaaggt 5942
|||||
601 CGAGACACTGCTCTGGGCTGTGCCACCAAGGCTCCAGAGAAAGTT 642

RESULT 11
LOCUS HSU85257 2000 bp mRNA PRI 19-MAR-1998
DEFINITION Human trabecular meshwork Inducible glucocorticoid response protein
(TIGR) mRNA, complete cds.
ACCESSION U85257
VERSION U85257.1 GI:2978428
KEYWORDS

SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2000)
AUTHORS Nguyen,T.D. and Polansky,J.R.
TITLE Glucocorticoid effects on HTM cells: Molecular Biology Approaches
JOURNAL Glaucoma Update 4, 331-343 (1991)
REFERENCE 2 (bases 1 to 2000)
AUTHORS Stone,F.W., Pingert,J.H., Alward,W.L.M., Nguyen,T.D.,
Polansky,J.R., Sundén,S.L.F., Nishimura,D., Clark,A.F., Nystuen,A.,
Nichols,B.E., Mackey,D.A., Ritch,R., Kalenak,J.W., Craven,E.R. and
Sheffield,V.C.
TITLE Identification of a gene that causes primary open angle glaucoma
JOURNAL Science 275 (5300), 668-670 (1997)
MEDLINE 97158493
REFERENCE 3 (bases 1 to 2000)
AUTHORS Nguyen,T.D., Chen,P., Huang,W.D., Chen,H., Johnson,D. and
Polansky,J.R.
TITLE Gene structure and properties of TIGR, an olfactomedin-related
glycoprotein cloned from glucocorticoid-induced trabecular meshwork
cells
J. Biol. Chem. 273 (11), 6341-6350 (1998)
MEDLINE 98165818
REFERENCE 4 (bases 1 to 2000)
AUTHORS Nguyen,T.D. and Polansky,J.R.
TITLE Direct Submission
JOURNAL Submitted (13-JAN-1997) Ophthalmology, University of California San
Francisco, 10 Kirkham Street, San Francisco, CA 94143, USA
5 (bases 1 to 2000)
AUTHORS Nguyen,T.D.
TITLE Direct Submission
JOURNAL Submitted (02-APR-1997) Ophthalmology, University of California San
Francisco, 10 Kirkham Street, San Francisco, CA 94143, USA
6 (bases 1 to 2000)
AUTHORS Nguyen,T.D.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1998) Ophthalmology, University of California San
Francisco, 10 Kirkham Street, San Francisco, CA 94143, USA
REMARK Sequence update by submitter
COMMENT On Mar 19, 1998 this sequence version replaced gi:1945067.
FEATURES
source 1..2000
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="primary cultured cells of trabecular meshwork
tissue"
/chromosome="1"
/map="1q23-q24"
/len=">2000
/gene="TIGR"
/len="37
/note="additional 5'UTR sequence deposited as TIGR gene
sequence with GenBank Accession Number AF007562"
37..1551
/gene="TIGR"
/codon_start=1
/product="trabecular meshwork inducible glucocorticoid
response protein"
/protein_id="AAC52051.1"
/db_xref="gi:1945068"
/translation="MRFCARCCSGEPMPAVOLLCLCYWDVNGARTAOIRKANDOS
GRCOYTFVSVPNESSCPQSQAMSVINILORDSSTORLDELATKARLSLESLHQL
TLDOARPOETQEGLORELGLRREDOLEOTRLESTVNSLNDKSVLEEKRLR
OENENLARLESSEQVLRGOCPTQRTDRAVAVPQSRVSTWNLDTLAFOELKSE
LVEVPARILKESPSGYLRSGEGDGCGLYVWGPPLTRTAETITGKVGWMDPKP
TYPKQETWRIIDVGTQVROVFEVDLISOVMGYPKSVHTLPLRLESTGAVVSGSL
YFOGAEKSTVIRIELNTETVAEKETIPAGKHGQPPYSMGCTTDLIDVDAGLMVIY
STDEAKGAIIVSKLNPENLEQIWEITWIRKQSVANATIGCTLTIVSSYTSADTVN
FAYDGTGISTLTITPFXNRYKSSMIDYNPLEKFLFAMDNLNMVYTDIKLSKM"
1552..>2000

3'UTR

/gene="TIGR"
/note="Additional 3'UTR sequence deposited as TIGR gene
sequence with GenBank Accession Number AF012654"
BASE COUNT 538 a 508 c 534 g 420 t
ORIGIN

Query Match 10.4% Score 640.4; DB 66; Length 2000;
Best Local Similarity 99.8%; Pred. No. 1,2e-129;
Matches 641; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5301 agagcttccagaggaagcctcaccagcctcgcgaatgaggtctctctgacgctgc 5360
DB 1 AGACCTTCCAGAGGAAGCCTCACCACCTCTGCAATGAGGTTCTTGTGACGTTGC 60
OY 5361 tgcagcttgagctgagatgacgctgctcagctgctgctgctgctgctgctg 5420
DB 61 TGCAGCTTTGGGCTTGAGATGCCAGCTGTCCAGCTGTGCTTGTGGCTGCTGGTGTGG 120
OY 5421 gatgtggggccagagacagctcagctcagagagcgaatgacagagctgagccag 5480
DB 121 GATGTGGGGCCAGAGACAGCTCAGCTCAGAGAGGCAATGACAGAGTGGCCGATGCCAG 180
OY 5481 tatacctcagctgctgagcagctcgaatgaaatccagctgctcagagagcagagccatg 5540
DB 181 TATACCTTCACTGTGGCCAGTCCCAATGAAATCCAGCTGCCAGAGCAGCAGCCATG 240
OY 5541 tcagtcacccaactac 5600
DB 241 TCAGTCACTCACTTAACCTTACAGAGACAGACACCAACCTTATGACTTGAGAGCCAC 300
OY 5601 aaagctcagctcagctcctcctgagagagctcctcaccacacacacacacacacac 5660
DB 301 AAAGCTCAGCTCAGCTCCTCTGAGAGCTCTCTCCACCAATGACTTGAGACAGCTGCC 360
OY 5661 aggcctcagagagacccagagagagctgcaagagagagctgagacacacacacacac 5720
DB 361 AGGCCCCAGAGACCCAGAGAGGCTGCAAGAGGAGCTGGCACCCTGAGCGGGAGCGG 420
OY 5721 gaccagcttgagaaac 5780
DB 421 GACCACTGGAACCCAAACCAAGAGAGTGGAGACTGCTTACAGCAACCTCTCCGAGAC 480
OY 5781 aagtcagcttcctgagagagagagagagcgaactaagcagaagaaatgaaatcctgagcag 5840
DB 481 AAGTCAGTTCGAGAGAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
OY 5841 aggttgagagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5900
DB 541 AGGTTGGAAGACAGCAGCAGCAGGAGGTAGCAAGCTGAGAGAGGAGGAGGAGGAGGAGGAGG 600
OY 5901 cgagacactgctcggtgctgctgctcaccagagctccagagagagct 5942
DB 601 CGAGACACTGCTCGGCTGTGCTGCACACAGCTCCAGAGAGATT 642

RESULT 12
LOCUS AB4847 2002 bp DNA PAT 21-JAN-2000
DEFINITION Sequence 2 from Patent WO9844108.
ACCESSION AB4847
VERSION AB4847.1 GI:6733711
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 2002)
AUTHORS Huang, W. and Nguyen, T. D.
TITLE DIAGNOSIS AND PROGNOSIS OF GLAUCOMA
JOURNAL Patent: WO 9844108-A 08-OCT-1998;
HUANG WEIDONG (US); NGUYEN THAI D (US)
FEATURES
Source Location/Qualifiers
1..2002

/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 538 a 508 c 535 g 421 t
ORIGIN

Query Match 10.4% Score 640.4; DB 5; Length 2002;
Best Local Similarity 99.8%; Pred. No. 1,2e-129;
Matches 641; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5301 agagcttccagaggaagcctcaccagcctcgcgaatgaggtctctctgacgctgc 5360
DB 1 AGACCTTCCAGAGGAAGCCTCACCACCTCTGCAATGAGGTTCTTGTGACGTTGC 60
OY 5361 tgcagcttgagctgagatgacgctgctcagctgctgctgctgctgctgctgctg 5420
DB 61 TGCAGCTTTGGGCTTGAGATGCCAGCTGTCCAGCTGTGCTTGTGGCTGCTGGTGTGG 120
OY 5421 gatgtggggccagagacagctcagctcagagagcgaatgacagagctgagccag 5480
DB 121 GATGTGGGGCCAGAGACAGCTCAGCTCAGAGAGGCAATGACAGAGTGGCCGATGCCAG 180
OY 5481 tatacctcagctgctgagcagctcgaatgaaatccagctgctcagagagcagagccatg 5540
DB 181 TATACCTTCACTGTGGCCAGTCCCAATGAAATCCAGCTGCCAGAGCAGCAGCCATG 240
OY 5541 tcagtcacccaactac 5600
DB 241 TCAGTCACTCACTTAACCTTACAGAGAGACAGACCAACCTTATGACTTGAGAGCCAC 300
OY 5601 aaagctcagctcagctcctcctgagagagctcctcaccacacacacacacacacac 5660
DB 301 AAAGCTCAGCTCAGCTCCTCTGAGAGCTCTCTCCACCAATGACTTGAGACAGCTGCC 360
OY 5661 aggcctcagagagacccagagagagctgcaagagagagctgagacacacacacacacac 5720
DB 361 AGGCCCCAGAGACCCAGAGAGGCTGCAAGAGGAGCTGGCACCCTGAGCGGGAGCGG 420
OY 5721 gaccagcttgagaaac 5780
DB 421 GACCACTGGAACCCAAACCAAGAGAGTGGAGAGTCTCTACAGCAACCTCTCCGAGAC 480
OY 5781 aagtcagcttcctgagagagagagagcgaactaagcagaagaaatgaaatcctgagcag 5840
DB 481 AAGTCAGTTCGAGAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
OY 5841 aggttgagagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5900
DB 541 AGGTTGGAAGACAGCAGCAGGAGGTAGCAAGCTGAGAGAGGAGGAGGAGGAGGAGGAGG 600
OY 5901 cgagacactgctcggtgctgctgctcaccagagctccagagagagct 5942
DB 601 CGAGACACTGCTCGGCTGTGCTGCACACAGCTCCAGAGAGATT 642

RESULT 13
LOCUS AB4850 2000 bp DNA PAT 21-JAN-2000
DEFINITION Sequence 2 from Patent WO9844107.
ACCESSION AB4850
VERSION AB4850.1 GI:6733713
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 2000)
AUTHORS Huang, W. and Nguyen, T. D.
TITLE DIAGNOSIS AND PROGNOSIS OF GLAUCOMA
JOURNAL Patent: WO 9844107-A 08-OCT-1998;
UNIVERSITY OF CALIFORNIA (US); HUANG WEIDONG (US)
FEATURES
Source Location/Qualifiers
1..2000
/organism="unidentified"

BASE COUNT 538 a 506 c 534 g 422 t
ORIGIN
Query Match 10.3%; Score 635.6; DB 5; Length 2000;
Best Local Similarity 99.4%; Pred. No. 1.4e-128;
Matches 638; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 5301 agagcttccagaggaagcctccaaagcctctgcaatgaggtctctgtgacgttgc 5360
DB 1 AGAGCTTCCAGAGGAGAGCCTTCACCAAGCCTTCGCAATGAGTCTCTGTCACGTTGC 60
QY 5361 tgaagctttgagctcagagcagcagctgctcagctctgtctgtgagctccggtgtg 5420
DB 61 TGAAGCTTTGAGCTCAGAGAGCAGCTGTCACCTGCTCTGTGAGCTGCTGTGTGG 120
QY 5421 gatgtgggagcagagcagctcagctcaggaagcgaatgacagagtggtgagcag 5480
DB 121 GATGTGGGGCCAGAGAGCTCAGCTCAGGAAGGCCAATACCAAGAGTGGCCATGCGAG 180
QY 5481 tatacctcagtggtgagcagctcccaatgaaatcagctgtccagagagcagcagccatg 5540
DB 181 TATACCTTCAGTGTGGCACTCCCAATGAATCCAGCTGCCAGAGCAGAGCCAGGCCATG 240
QY 5541 tcaagtatccataacttaccagagagacagacacccaagcttagagctgagggccacc 5600
DB 241 TCAGTATCCATTAAGTACAGAGAGAGAGAGAGCCCAAGCTTAGACCTGAGAGGCCACC 300
QY 5601 aaagctcagactcagctccctctgagagcctcctcccaatctgagcagcagctgccc 5660
DB 301 AAAGCTTCAGTACGCTCCCTGAGAGAGCTCTCCACCAATTGACCTTGAGACAGGCTGCC 360
QY 5661 aggcctcagagagacccagagagggctgagagggagctgagcagccttgaagcggagcgg 5720
DB 361 AGGCCCCAGAGAGACCCAGAGGGGCTGCAAGAGGAGCTGGGACCCCTGAGGCGGAGCGG 420
QY 5721 gaccacactggaagacccaaacagagagtgagagactgtctacagcaacccctcccgagac 5780
DB 421 GACCACCTGGAAGACCCAAACAGAGAGTGTGAGAGCTGCTTACAGCAACCTCTCCGAGAC 480
QY 5781 aagctcagctcagagagagagagagcagactaagcagaagaaatgagaaatctgagcagc 5840
DB 481 AAGCTCAGTGTGAG 540
QY 5841 aggttgagagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5900
DB 541 AGGTTGGAAG 600
QY 5901 cgagacacagctcagcagctgctgctgctgctgctgctgctgctgctgctgctgctgct 5942
DB 601 CGAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 642
RESULT 14
LOCUS HSAF001620 2061 bp mRNA PRI 03-SEP-1997
DEFINITION Homo sapiens trabecular meshwork-induced glucocorticoid response
ACCESSION AF001620
VERSION AF001620.1 GI:2104788
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Escribano, J., Ortego, J. and Coca-Prados, M.
TITLE Isolation and characterization of cell-specific cDNA clones from a
human donor: transcription and synthesis of plasma proteins
JOURNAL J. Biochem. 118 (5), 921-931 (1995)
MEDLINE 96318503

REFERENCE 2 (bases 1 to 2061)
AUTHORS Stone, E.M., Fingert, J.H., Alward, W.L.M., Nguyen, T.D.,
Polansky, J.R., Sundén, S.L.F., Mishimura, D., Clark, A.F., Nystuen, A.,
Nichols, B.E., Mackey, D.A., Ritch, R., Kalenak, J.W., Craven, E.R. and
Sheffield, V.C.
TITLE Identification of a gene that causes primary open angle glaucoma
JOURNAL Science 275 (5300), 668-670 (1997)
MEDLINE 97158493
REFERENCE 3 (bases 1 to 2061)
AUTHORS Ortego, J., Escribano, J. and Coca-Prados, M.
TITLE Cloning and characterization of subtraced cDNAs from a human
ciliary body library encoding TIGR, a protein involved in juvenile
open angle glaucoma with homology to myosin and olfactomedin
JOURNAL FEBS Lett. 413 (2), 349-353 (1997)
MEDLINE 97424389
REFERENCE 4 (bases 1 to 2061)
AUTHORS Coca-Prados, M., Ortego, J. and Escribano, J.
TITLE Direct Submission
JOURNAL Submitted (29-APR-1997) Ophthalmology and Visual Science, Yale
University School Medicine, 330 Cedar St. New Haven, CT 06520, USA
FEATURES
source location/Qualifiers
1..2061
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1q21-q31"
/issue_type="ocular ciliary body"
1..2061
/gene="TIGR"
/note="Putative gene for juvenile open angle glaucoma"
23..1537
/gene="TIGR"
/codon_start=1
/product="trabecular meshwork-induced glucocorticoid
response protein"
/protein_id="AAC51725.1"
/db_xref="GI:2104789"
translation="MRFCARCCSGPMPAYOLLILACLVMDGAPTAOLRKANDOS
GRQYTFVAFSPNESCPEQSQAMSVHINLODSTORUDLEATRAIRLSLESLHOL
TIDQARPOETEGLORELCTRRRDQLEOTRLETRAYSLLDKSYLEBEKRLR
QENELARLESSQGVARLRGQCPQRTDARAVPDSREYVSNLDTLAFQELKSE
LNEVASRLKESPSGYLRSGEGDGLVWVGEPYLRLAETITGKYGVMRDPK
TYPYQETWRIDTGVDRQVFEYDLISQFQGPVSKVHILPRLSESTGAVYSGSL
YFGAESRTVIRELNTETVKAKEKIPGKYGQPSMGVYDIDLAVDEAGLWVY
SDPEAKAIVLSKLNPELLEOTETNIRSVSNAPFLICGLTVTSYSADATVN
RAYDGTGSKTLTTPFNKRYSSMIDNPLEKRLFAMDNLMTYTIKLSKM"
BASE COUNT 570 a 517 c 537 g 437 t
ORIGIN
Query Match 10.2%; Score 626.4; DB 66; Length 2061;
Best Local Similarity 99.8%; Pred. No. 1.4e-126;
Matches 627; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5315 gaagcctcacaagcctctgcaatgaggtctctgtgacagctgtgacagcttgggccc 5374
DB 1 GAAGCCTCACAGAGCCTTCGCAATGAGGTTCTCTGTGACAGCTGTGACAGCTTTGGGCC 60
QY 5375 tgaagtgccagcagctgctcagctgctctgtgagcctggtgtgagtgatggggccag 5434
DB 61 TGAAGTGCCAGCTGTCACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
QY 5435 gacagctcagctcaggaagcgaatgacagagtggtgagcagctgacatatactcagtg 5494
DB 121 GACAGCTCAGCTCAGGAAGGCCAATAGACAGATGGCCATGCTCACTATACCTTCAGTGT 180
QY 5495 ggcacgtcccaatgaaatccagctgcccagagcagagcagcagcagcagcagcagcagc 5554
DB 181 GGCAAGTCCCAATGAAATCCAGCTGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 5555 ctacagagagacagagacacccaagccttagaccttgagggccacaagaagctgactcag 5614
DB 241 CTACAG 300

Oy 5615 cccccgagagagcctccaccacaaatgaccttgagaccagagctgcagagccccagagagac 5674
Db 301 CTCCTGGAGAGCTCTCTCCACCAATTGACCTTGGACACAGGCTGCCAGAGCCCCAGAGAC 360
Oy 5675 ccaagagagagctgcaagagagctggaacccctgagcgagcgagagccagctggaac 5734
Db 361 CCAGAGAGGGCTGCAGAGAGGACTGGGACCTGTAGAGGGGAGCGGAGCACACTGGAAC 420
Oy 5735 ccaaacccagagagcttgagagagctgctacagacacccctcctcgagagcaagctcctga 5794
Db 421 CCAAACCCAGAGAGTGGAGACTGCTACAGCAACCTCCCGAGACAGTCACTCTGA 480
Oy 5795 ggaagagagagagagcagcacaagcaagaaatgagaatctgagccagagagcttgagagagc 5854
Db 481 GGAAGAGAGAGAGCCACTTAAGGCAAGAAATAGAAATCTGGCCAGAGAGTTGGAAGCAG 540
Oy 5855 cagccagagagtagcaagagcttgagagagggccagctgcccagagaccgagacactgctcg 5914
Db 541 CAGCCAGAGAGTAGCAAGGCTGAGAAAGGGCCAGTGTCCCGAGACCCGAGACACTGCTCG 600
Oy 5915 ggcctgcccagagagctccagagaggt 5942
Db 601 GGCCTGCCACAGGCTCCAGAGAGTT 628

RESULT 15

AB4848 LOCUS AB4848 1512 bp DNA PAT 21-JAN-2000
DEFINITION Sequence 3 from Patent WO9844108.
ACCESSION AB4848
VERSION AB4848.1 GI:6733712
KEYWORDS

SOURCE unidentifed.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 1512)
AUTHORS Huang, W. and Nguyen, T. D.
TITLE DIAGNOSIS AND PROGNOSIS OF GLAUCOMA
JOURNAL Patent: WO 9844108-A 08-OCT-1998;
HUANG WEIDONG (US); NGUYEN THAI D (US)
FEATURES Location/Qualifiers

source 1..1512
/organism="unidentifed"
/db_xref="taxon:32644"
BASE COUNT 392 a 406 c 423 g 291 t
ORIGIN

Query Match 9.8%; Score 604.4; DB 5; Length 1512;

Best Local Similarity 99.8%; Pred. No. 8.5e-123;

Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 5337 atgaggtctctctgcaagctgctgacagcttgagcctgagatgacagctgtccagctg 5396
Db 1 ATGAGGTCTCTCTGCAAGTGTGCAAGCTTGGGCTGAGATGCCAGCTGTCCAGCTG 60
Oy 5337 ctgctctcgagctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 5456
Db 61 CTGCTTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Oy 5457 aatgacagagctgagcagctgacagctgacagctgacagctgacagctgacagctgacagc 5516
Db 121 AATGACAGAGAGGCGCATGCGATATACCTTCAAGTGTGCGCAGTCCCATGATCCAGC 180
Oy 5517 tgcacagagcagagcagagcagctgacagctgacagctgacagctgacagctgacagc 5576
Db 181 TGCCAGAGCAGAGCCAGGCGCATGCTAGTCAATCACTTAAGAGAGAGAGAGAGAGCAGC 240
Oy 5577 caagcttagacctgagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5636
Db 241 CAAGCTTAGACCTGAGAGCCAGCAAGAGCTGAGTCACTGAGAGAGCTGAGAGAGCTCTCCAC 300

Oy 5637 caatgaccttgagaccagagctgcccagagcagagagaccagagagagctgcaagagagag 5696
Db 301 CAATGACCTTGGAGACAGAGCTGCCAGGCCCAAGAGACCCAGAGAGGGCTGCAGAGGGAG 360
Oy 5637 ctggaacccctgagagcgagagcgagagcagctggaaccccaaccagagagcttgagagct 5756
Db 361 CTGGACACCTGAGAGCGGAGCGGAGCCAGCTGMAACCAACAGAGAGTTGAGACT 420
Oy 5757 ggcctacagacacccctcctccagagacagctcagcttctgagagagagagagagcagactaag 5816
Db 421 GCTTACAGCAACCTCTCTCGAGACAGTCAAGTCTGAGAGAGAGAGAGAGAGAGTAAAG 480
Oy 5817 caagaaatgagaaatctgagcagagagcttgagaaagcagcagcagagagtagcaagagctg 5876
Db 481 CAAGAAATGAGAAATCTGCGCAGAGAGTTGGAAGAGCAGACAGAGAGTAGCAAGGCTG 540
Oy 5877 agaaagggcagctgtcccaagacccagagacacactcctcgagctgtgccaagagctcaga 5936
Db 541 AGAAGGGCCAGTGTCCCGAGAGCCGAGACACTGCTCGGCTGTGCCACAGGCTCCAGA 600
Oy 5937 gaaggt 5942
Db 601 GAAGTT 606

Search completed: December 3, 2000, 18:35:10
Job time: 43924 sec

•
•
•
•